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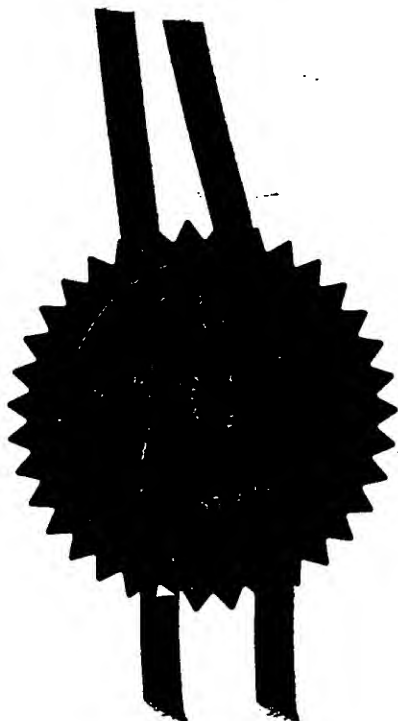
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**The
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Form 1/77

Patents Act 1977

① Title of invention

1 Please give the title
of the invention GENE PRODUCT AND METHOD

② Applicant's details

☐ First or only applicant

2a If you are applying as a corporate body please give:

Corporate name ISIS INNOVATION LIMITED

Country (and State
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appropriate) United Kingdom

2b If you are applying as an individual or one of a partnership please give in full

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2c In all cases, please give the following details:

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please give details below

Agent's name Stevens, Hewlett & Perkins

Agent's address 1 Serjeants' Inn
Fleet Street
London

Postcode EC4Y 1LL

Agent's ADP
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15(4) (Divisional) ☐ 8(3) ☐ 12(6) ☐ 37(4) ☐

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8a Please fill in the number of sheets for each of the following types of
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Continuation sheets for this Patents Form 1/77

Claim(s)

3

Description

21

Abstract

Drawing(s)

15

8b Which of the following documents also accompanies the application?

Priority documents (please state how many)

Translation(s) of Priority documents (please state how many)

Patents Form 7/77 - Statement of Inventorship and Right to Grant
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Patents Form 9/77 - Preliminary Examination/Search

Patents Form 10/77 - Request for Substantive Examination

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GENE PRODUCT AND METHOD

Introduction

The present invention relates to proteins, polypeptides, nucleic acid fragments, antibodies and related products and to their use in medicine and agriculture, for instance in diagnosis and therapy. More particularly the invention relates to a gene or genes which control the sex of the embryos of birds and to their use in ascertaining the sex of cells, embryos and tissues and controlling the sex of the progeny of birds

Much of our understanding of sex determination comes from three, extensively studied, model systems. In two of these, the fruitfly *Drosophila melanogaster* and the nematode *Caenorhabditis elegans*, it is the ratio of X chromosomes to autosomes that initiates sexual differentiation [Hodgkin, 1992 #435]. In the mouse a single gene, *sry*, located on the Y chromosome provides the impetus for male development; a pattern that is thought to be conserved throughout the mammals [Koopman, 1991 #319 Foster, 1992 #323].

At the genetical level these three species employ very different molecular mechanisms, not only to control sex determination itself but to accommodate the differing dosages of genes that result from the males possessing a single X and the female two X chromosomes. These basic differences are largely due to the independent evolution of the three mechanisms and strongly suggests that other means of sex determination will have evolved elsewhere in the animal kingdom.

One class in which little is known about sex determination is the birds. They exhibit female heterogamety which means that the female has Z and W sex chromosomes and the male ZZ. This immediately suggests that sex determination in this class has an independent origin to that of their sister class, the mammals where it is the male that is heterogametic. Furthermore, it has been shown that whilst female mammals inactivate one of their X chromosomes as a method of dosage compensation [Grant, 1988 #449], this does not seem to be a device employed by birds [Baverstock, 1982 #102].

However, similarities do exist between the birds and mammals. The W chromosome, like the Y chromosome is usually smaller than its partner, and is also characteristically heterochromatic in appearance [Christidis, 1990 #440]. The main exceptions to this rule are found in the 'primitive' representatives of both classes: the monotremes and the ratites where the morphological differences between the sex chromosomes are poorly defined [Graves, 1987 #408; Tagaki, 1972 #205].

The heterochromatization of the W and Y results from the replacement of functional genetic loci with junk DNA sequences. This process is thought to be a consequence of a suppression of recombination that has arisen to ensure that genes vital to the development of the heterogametic sex remain linked on the Y or W chromosome [Charlesworth, 1991 #407]. As a result only a few genes such as *Ube1y* [Kay, 1991 #328; Mitchell, 1991 #327], *Zfy* [Page, 1987 #322] and *SRY* itself remain on the mammalian Y chromosome. A similar situation is thought to prevail on the avian W chromosome where the presence of any functional genes has yet to be demonstrated, although it does possess vast arrays of repetitive elements [Tone, 1982 #178; Griffiths, 1990 #77].

A further similarity in sex determination in birds and mammals is that the development of the male phenotype appears crucially dependent on the appearance of the testis. The female phenotype is the result of the 'default pathway'. For mammals this was first demonstrated by Jost (1947) who grafted an embryonic testis into genetically female rabbit embryos prior to sex determination. This was sufficient to allow the development of functional males. The same experiment has been carried out on chick embryos [Stoll, 1978 #451] with comparable results.

Once the testis has formed, the process of masculinization is adopted by the testicular hormones. The genetical switch that initiates testis determination is known to be *SRY* in mammals [Koopman, 1991 #319]. In birds, there appears to be no *SRY* homologue on the W chromosome [Griffiths, 1991 #78], although this is unsurprising given the separate evolution of sex determination in the two classes.

The only other pertinent evidence on the genetics of avian sex determination come from reports of chickens with abnormal chromosome complements. Table 1 shows data from [Crew, 1954 #450] and [McCarrey, 1979 #448] on the phenotypes of the aneuploids so far described. These results suggest that the presence of the W chromosome in the aneuploid AA ZZW and the polyploid AAA ZZW has not acted as a dominant determinant of the female phenotype. This may mean that sex in birds may be determined more by the autosome to Z ratio, as in *Drosophila* and *C. elegans*. However, a ZO aneuploid which could confirm this hypothesis has yet to be described.

It must also be born in mind that XXY kangaroos, where *SRY* is thought to be the key male determining switch, exhibit both male and female characteristics [Graves, 1987 #408]. This suggests that the limited aneuploid data that is available for birds should be interpreted with some caution.

To conclude, the genetic mechanism that controls sex determination in birds has not yet been elucidated. In this paper we suggest that a gene we have termed *CHD-W* (Chromodomain-Helicase-DNA binding on the *W* chromosome) alone or acting in conjunction with a closely related gene *CHD-1A* (Chromodomain-Helicase-DNA binding 1 Avian) initiates female development in birds.

It is believed that the all birds such as chickens and other species of commercial significance, will have two or more genes of the CHD type which will have a nucleotide sequence similar to the nucleotide sequences shown in fig. 5, fig. 7 and fig. 8 and that the gene products will be proteins which are crucial to the determination of the sex of the organism. One of these genes will be located on the *W* chromosome and the other on an autosome or *Z* chromosome.

It will be understood that the exact sequence of the two genes will vary between species and between individuals of the same species at least at the nucleotide level and often also at the protein level. Partial sequences of the chicken genes are shown in fig. 5, fig. 7 and fig. 8. The gene or protein which contains sequence corresponding to those in fig. 5, fig. 7 and fig. 8 will hereafter be referred to as an CHD-gene and proteins and fragments thereof, polypeptides, nucleic acids and fragments thereof and oligonucleotides containing part of a CHD gene will hereafter be referred to as CHD-proteins, CHD-nucleic acids and so on.

The present invention therefore provides a CHD-protein or a fragment thereof or polypeptide comprising a CHD-gene or a part thereof, subject to the proviso below.

The present invention also provides a protein or a fragment thereof or a polypeptide containing a mimotope of an epitope of a CHD-protein or fragment thereof of polypeptide containing a CHD-gene or a part thereof, subject to the proviso below. Such proteins, fragments and polypeptides are hereafter referred to as CHD-mimotope proteins or fragments thereof and mt-mimotope polypeptides.

The present invention also provides a CHD-nucleic acid or a fragment thereof or oligonucleotide comprising a CHD-gene, or a part thereof subject to the proviso below.

In a particular aspect the present invention provides a single or double stranded nucleic acid comprising the CHD-gene of a bird or a part thereof of at least 17 contiguous nucleotide bases or base pairs, or a single or double stranded nucleic acid hybridizable with the CHD-gene of a bird, or part thereof of at least 17 contiguous nucleotide bases or base pairs, subject to the proviso below.

The invention further provides a nucleic acid or fragment thereof or an oligonucleotide encoding a CHD-protein or fragment thereof or a polypeptide comprising a CHD-gene or a

part thereof or a CHD-mimotope protein or a fragment thereof or CHD-mimotope polypeptide subject to the following proviso. These nucleic acids, fragments and oligonucleotides may have sequences differing from the sequences of CHD-nucleic acids, fragments and oligonucleotides due to alternative codon usage and/or encoding alternative amino acid sequences or mimetopes.

The present invention does not, however extend to any known protein or fragment thereof or polypeptide or nucleic acid or fragment thereof or oligonucleotide containing a CHD-gene related sequence such as the *Saccharomyces cerevisiae* SNF2/SWI2 gene, *Drosophila polycomb* and HP1 genes described below, insofar as that protein or fragment, polypeptide, nucleic acid or fragment or oligonucleotide is known *per se*.

The amino acid sequence of the CHD-gene has similarities to the chromobox and helicase motifs of a number of known genes known to be involved in the remodelling of chromatin. This suggests that the CHD-protein of the present invention may have a regulatory function involving chromatin remodelling. However, none of these genes contain the chromobox and the helicase of the CHD-gene which are conserved in conjunction, at least in the chicken, great tit, mouse and yeast but are not conserved in conjunction in the sequences of chromatin remodelling proteins not associated with sex determination at least at the stage of testis formation in birds. A protein having chromatin remodelling capacity but lacking these characteristic motifs is therefore outside the scope of the present invention.

In addition there are certain residues in the amino acid sequence of the chromobox and those residues immediately downstream thereof, of the CHD-gene which are also conserved at least between those found in the chicken, great tit, mouse and yeast but are not conserved in the sequences of chromatin remodelling proteins not associated with sex determination at least at the stage of testis formation in birds. Any one of these conserved residues is therefore considered characteristic of the CHD-gene proteins of the present invention. A protein having chromatin remodelling capacity and a helicase motif but lacking all or most of these characteristic amino acid residues in the chromobox motif is therefore outside the scope of the present invention.

The characteristic amino acid residues are shown in the alignment in fig. 11, which is described in more detail below. When aligned with the illustrated sequences as shown, these residues fall at positions, 11,12, 20, 27, 34 inside the chromobox and 3, 6, 8, 12-15, 16 immediately downstream.

The nucleotide base sequence of the CHD-gene includes bases which encode the chromobox and helicase motifs of chromatin remodelling proteins as described above. However, the base sequence of the CHD-nucleic acids of the gene will include codons specifying both chromobox and helicase motifs and the former will have codons specifying one or more of the characteristic amino acid residues described above and/or will be hybridizable with a sequence that controls the sex determination of birds under conditions which substantially prevent hybridization to other sequences in birds that do not have these characteristics.

Preferably the CHD-nucleic acids of the invention encode a chromobox and a helicase and one or more, preferably all, of the characteristic chromobox amino acid residues and meet the above hybridization requirements.

Fragments of CHD-nucleic acids according to the present invention will likewise contain codons specifying the chromobox and helicase motifs or including at least part of either of these motifs or CHD-gene adjacent to the codons encoding these features and/or will be hybridizable with a sequence that controls the sex determination of birds under conditions which substantially prevent hybridization to other sequences in birds that do not have these characteristics.

Oligonucleotides containing the CHD-gene or a part thereof according to the present invention may contain codons specifying the chromobox or helicase motifs or including at least part of these motifs or CHD-gene but this is not essential. However all such oligonucleotides of the invention must be capable of hybridizing with a sequence or sequences that control the sex determination of birds, preferably under conditions which substantially prevent hybridization with any sequence not associated with sex determining sequence.

The sex determining sequences referred to herein is the sequence which contains the CHD-gene and which encodes a factor which when expressed at the appropriate stage and level during embryo development may result in testis formation and subsequent growth of the embryo as a male. It may alternatively refer to the sequence which encodes a factor which when expressed at the appropriate stage and level during embryo development prevents testis formation and results in the subsequent growth of the embryo as a female.

The hybridization conditions referred to above which prevent unwanted hybridization with sequences not associated with the sex determining gene will depend to some extent on the length of the nucleic acid, fragment or oligonucleotide of the invention tested. Thus for instance lower stringency will be sufficient to secure hybridization to sequences associated with the sex

determining gene whilst preventing unwanted hybridization when the nucleic acid or fragment is several thousand nucleotide base pairs in length than for a fragment of only a few hundred bases or an oligonucleotide of from 17 bases up to a few tens or hundreds of bases. With the smallest oligonucleotides and fragments of the invention hybridization conditions will be such that only complete complementarity between the oligonucleotide and or fragment and the sequences associated with the sex determining gene will result in hybridization.

Preferred nucleic acids and fragments of the invention will only hybridize selectively to the sequences associated with the sex determining gene or genes under conditions requiring at least 80%, for instance 85, 90 or even 95% or preferably 99% complementarity. Yet more preferred nucleic acids and fragments of the invention are those having a sequence corresponding exactly to that of those illustrated in fig. 5, fig. 7 and fig. 8 although the nucleotide sequences may be longer or shorter than those illustrated and or may contain normally intronic sequences associated with these sequences

The invention particularly provides an oligonucleotide, polypeptide, nucleic acid or protein comprising the entire sequence of the CHD-gene of a bird and more preferably comprising the entire amino acid or nucleotide sequence of the chicken as set out in any one of figs 1, 3, 5, 7, 8, 9, 10, 11.

The nucleic acids hybridizable with the CHD-gene of a bird are preferably hybridizable under moderate, or more preferably, high stringency conditions as defined below:

Moderate stringency:

Buffer:	2 x SSC
Temp:	50°C
Annealing period:	6-8hrs

High stringency:

Buffer:	1 x SSC
Temp:	65°C
annealing period:	6-8hrs

Moderate stringency as defined above corresponds with about 75% homology. High stringency as defined above corresponds with about 90% homology. 1 xSSC is 0.15 M sodium chloride, 0.015 M sodium citrate, pH 7.0.

Preferably the portion of the nucleic acid corresponding to or hybridizable with the CHD-gene is at least 20, more preferably at least 30, 40 or 60 and most preferably 100 or more nucleotide bases in length.

The nucleotide strands of the invention may be single or double stranded DNA or RNA. DNA's of the invention may comprise coding and/or non-coding sequences and/or transcriptional and or translational start and/or stop signals and/or regulatory, signal and/or control sequences such as promoters, enhancers and/or polyadenylation sites, endonuclease restriction sites and/or splice donor and/or acceptor, in addition to the CHD-gene sequence. Included within the DNA's of the invention are genomic DNA's and complementary DNA's (cDNA's) including functional genes or at least an exon containing the CHD-gene. They may also contain non-coding sequences such as one or more introns. Single stranded DNA may be the transcribed strand or the non-transcribed (complementary) strand. The nucleic acids may be present in a vector, for instance a cloning or expression vector, such as a plasmid or cosmid or a viral genomic nucleic acid. RNA's of the invention include unprocessed and processed transcripts of DNA, messenger RNA (mRNA) containing the CHD-gene and anti-sense RNA containing a sequence complementary to the CHD-gene.

Nucleic acids of the present invention are particularly useful as primers for polymerase chain reactions (PCRs) conducted to ascertain the sex of a bird as defined below. They may also be used to express proteins or fragments or polypeptides corresponding to the whole or a part of a CHD-protein (whether or not containing a CHD-gene) or as probes in hybridization experiments. As used herein the term "fragments" used in connection with proteins is intended to refer to both chemically produced and recombinant portions of proteins.

The CHD-proteins and fragments thereof and polypeptides containing the CHD-gene or a part thereof and CHD-mimotope proteins and fragments thereof and CHD-mimotope polypeptides of the invention are useful in immunodiagnostic testing and for raising antibodies such as monoclonal antibodies for such uses. Antibodies against such proteins and fragments and polypeptides as well as fragments of such antibodies (which antibody fragments include at least one antigen binding site) including chemically derived and recombinant fragments of such antibodies, and cells, such as eukaryotic cells, for instance hybridomas and prokaryotic recombinant cells capable of expressing and, preferably secreting antibodies or fragments thereof against such proteins or fragments, also form part of the present invention.

The nucleic acids of the invention may be obtained by conventional means such as by the recovery from organisms using PCR technology or hybridization probes, by *de novo* synthesis

or a combination thereof, by cloning the CHD-nucleic acids described below or a fragment thereof or by other techniques well known in the art of recombinant DNA technology.

Proteins and fragments thereof and polypeptides of the invention may be recovered from cells of organisms expressing a CHD-gene or generated by expression of a CHD-gene or coding sequence contained in a nucleic acid of the present invention in an appropriate expression system and host, or obtained by *de novo* synthesis or a combination thereof, by techniques well known in the art of recombinant DNA technology. The proteins, fragments thereof and polypeptides of the invention will contain naturally occurring L- α -amino acids and may also contain one or more non-naturally occurring α -amino acids having the D- or L-configuration

Antibodies may be obtained by immunization of a suitable host animal and recovery of the antibodies, by culture of antibody producing cells obtained from suitably immunized host animals or by *in vitro* stimulation of B-cells with a suitable CHD-protein, fragment or polypeptide or CHD-mimotope, protein, fragment or polypeptide and culture of the cells. Such cells may be immortalized as necessary for instance by fusion with myeloma cells. Antibody fragments may be obtained by well known chemical and biotechnological methods.

All these techniques are well known to practitioners of the arts of biotechnology. Reference may particularly be made to the well known text book "Molecular cloning: A laboratory manual" 2nd Edition (Eds Sambrook, J., Fritsch, E.F. and Maniatis, T.), (Cold Spring Harbour Laboratory, New York, 1989), hereafter referred to as "Maniatis".

The invention further provides the use of a nucleic acid, protein, polypeptide, antibody, or antibody producing cell as hereinbefore defined including the SNF2/SWI2, polycomb and HP1 or other chromobox or helicase containing protein for ascertaining the sex of a cell or organism of a bird or for isolating nucleic acids useful in ascertaining the sex of a bird and for instituting single sex breeding programmes.

Knowledge of the chicken or great tit sex determining gene or genes can be used to isolate the equivalent gene or genes from other birds. Once isolated from a particular species, this gene or genes and its sequence can be used in two types of application:

1. The construction of sequence based sexing tests which can be applied to embryos, tissues and other biological materials containing nucleic acids.

2. The genetic modification of the germ line of birds to create breeding systems that produce offspring statistically biased towards one sex or of one sex only (single sex breeding systems).

A particularly preferred technique for ascertaining the sex of a bird in accordance with the invention involves the use of an oligonucleotides as primers in a PCR, for instance as follows:

A cell or cells or remains thereof are obtained, for instance by surgical removal from an embryo or from the quill of a feather, and the DNA is released by a crude lysis procedure for instance using a detergent or by heating. Primer oligonucleotides of the invention are used to initiate a conventional PCR in order to amplify W chromosome linked CHD-related DNA from the cells. The products of the PCR are analysed by agarose gel electrophoresis and detected using labelled probes or by visual inspection. The presence of amplified DNA indicates the presence of a *CHD-W* gene in the cells and thus, in birds, that the cell(s) were female.

This technique may be applied for instance to identify the sex of embryos or adults for subsequent breeding programs, or to control the sex of the progeny of breeding stock for commercial exploitation (by selection of the breeding stock or by slaughter or termination of animals of undesired sex).

The oligonucleotide primers for ascertaining or controlling sex in one species may also be used to ascertain or control sex in another species since hybridization of the primers to the CHD-gene of the other species will still serve to amplify the species-specific sequences.

Techniques for conducting such determinations are well known in the art of recombinant DNA technology.

In one aspect the present invention provides a process for isolating a W-chromosome specific sequence associated with the *CHD-W* gene of a bird which comprises probing a genomic library from a female of the species preferably of W chromosome sequences, for instance of lambda phage, cosmid or YAC library or cDNA library constructed from a tissue expressing the gene, with a probe comprising a nucleic acid, fragment or oligonucleotide of the invention as hereinbefore defined and a detectable label under high or moderate stringency.

Using the newly isolated subclone, Southern blots are performed on male and female DNA of the species of interest at high stringency to confirm that the correct clone has been isolated. The CHD-gene probe should give a female specific signal (other male/female shared bands may also be present at lesser intensities). The subclone is sequenced using standard methods and primers suitable for PCR chosen from the sequence so identified.

Alternatively, other approaches to cloning the sequences related to the sex determining gene could be used such as PCR methods using "degenerate" oligonucleotides. (For methods in PCR see, for example, "PCR Protocols - a Guide to Methods and Application"; edited by M.A. Innis, D.H. Gelfand, J.J. Sninsky, T.J. White; published by Academic Press, Inc.).

Preferably the probe is *CHD-1A* or *CHD-W* or a fragment thereof or a nucleic acid or fragment or oligonucleotide having a sequence exactly as set out in Fig. 5, fig. 7 or fig. 8 for the chicken. Techniques for forming a genomic or cDNA library and for probing and detecting the detectable label and isolating the nucleic acid identified by the probe are well known in the art of biotechnology and recombinant DNA manipulation. The process may be conducted for instance using a probe having the chicken sequence such as the *CHD-W* sequence to identify and isolate the corresponding sequence from another bird such as Turkey. The thus-identified sequence can then be used to generate primers for PCR which in turn can be used to ascertain the sex of an individual or of cells, tissues, embryos or ovaries of the bird. This will permit experiments to ascertain sex to be conducted and controlled sex breeding of the bird as described below.

The isolated nucleic acid, fragment or oligonucleotide may thereafter be amplified, cloned or sub-cloned as necessary. The invention further provides a process for detecting the sex of an individual bird or of cells, tissues, embryos, foetuses or ovaries or a bird, comprising conducting a polymerase chain reaction using DNA from the individual, cell, tissue, embryo or ovary as template and a nucleic acid, fragment or oligonucleotide of the invention as primer. Preferably the nucleic acid, fragment or oligonucleotide of the invention used as primer is *CHD-W* or *CHD-1A* or a part thereof and has a sequence corresponding exactly to the chicken sequence in fig. 5, fig. 7 or fig. 8 or a part thereof or is a nucleic acid, fragment or oligonucleotide which is a W-chromosome specific sequence associated with the sex determining gene or genes of a bird of the same species as the individual cell, tissue, embryo, foetus or ovary whose sex is to be ascertained. The W-chromosome specific sequence associated with the sex determining gene or genes of the bird involved may itself have been obtained by the process of isolation and amplification or cloning described above.

The identification of the sex determining gene or genes according to the present invention raises the possibility of controlling the sex of progeny of commercially important animals such as chickens, turkeys and other avians. This will be valuable in many aspects of animal breeding and husbandry such as where one sex has more desirable characteristics, for instance only female progeny are desired for egg-laying breeds of chicken. The economic advantages of single sex breeding programmes and strategies for instituting these are described for instance in

"Exploiting New Technologies in Animal Breeding; Genetic Developments", (Eds. Smith, C., King, J.Q.B. and McKay, J.C.), (Oxford University Press, Oxford, 1986).

The nucleic acids making up all or part of the sex determining gene, from the same or different animal species, can be introduced into any early embryo through established transgenic technology. This latter includes microinjection of DNA into pronuclei or nuclei of early embryos, the use of retroviral vectors with either early embryos or embryonic stem cells, or any transformation technique, (including microinjection, electroporation or carrier techniques) into embryonic stem cells or other cells able to give rise to functional germ cells. These procedures will allow the derivation of individual transgenic animals (founder transgenics) or chimeric animals composed in part of cells carrying the introduced DNA. Where the functional germ cells of the founder transgenic or chimeric animal carry the introduced DNA it will be possible to obtain transmission of the introduced DNA to offspring and to generate lines or strains of animals carrying these DNA sequences.

The nucleic acids making up part or all of the coding sequence of the sex determining gene, or derivatives of it, may be introduced in combination with its own regulatory sequences (promoter/enhancers *etc.*) or regulatory sequences from another gene, the whole making the "construct", to give expression from the construct at an appropriate developmental stage and tissue location critical to sex determination in the bird species under consideration. For example, in the chicken this would be between 6 and 7 days post lay.

Materials and Methods

Isolation of pGT-W, pGT1.7 and pGT8

A great tit (*Parus major*) library was constructed from genomic DNA, partially restricted with *Mbo*I, and the lFixII vector (Stratagene). The library was screened at high stringency with the 724bp probe (GT-W) cloned from a W chromosome specific polymerase chain reaction (PCR) product derived from the great tit [Griffiths, 1993 #379]. Positive plaques were subject to two rounds of purification. Clone lGT2 contained an insert of 9.6kb that hybridized strongly to the probe sequence. The insert was subcloned as two *Eco*RI fragments of 1.7kb (pGT1.7) and 8kb (pGT8) into *Eco*RI cut pT7/T3 (Pharmacia).

Isolation of CHD genes from the chicken

Two chicken cDNA libraries were screened. The first was a mixed sex chick stage 10-12 cDNA library in lZapII which had been reamplified on 2 occasions. This library was provided by Dr I.J. Mason. The second library was constructed from mixed sex, 10 day chick mRNA. Total RNA was extracted using a guanidine thiocyanate based technique [Koopman, 1993

#550] and mRNA isolated using a Promega PolyATtract system 1000. A lZapII library was constructed using a Stratagene ZAP-cDNA synthesis kit.

Plaques (2×10^5) from the stage 10-12 day library were screened at moderate stringency with a subcloned 433bp HindIII/SacI fragment from pGT8 that contained the 123bp region with identity to the mouse *CHD-1* gene [Delmas, 1993 #415]. A similar number of plaques from both libraries were screened with bases 122-4132 of *CHD-1A* (see fig. 5). The 10 day library was also screened with bases 3763-5007 of *CHD-1A* (see fig. 5). Positive plaques were purified prior to the excision of pBluescript plasmids and cloned inserts insert from lZapII using techniques recommended by Stratagene.

Sequencing

All sequencing was carried out using the T7 DNA polymerase/7-deaza-dGTP chain termination sequencing kit from USB. All sequencing unless otherwise specified was carried out in both directions either by subcloning or through exonuclease III deletion with the Promega Erase-a-Base system.

Southern Blot Analysis and Hybridization

Genomic DNA was extracted from blood [Griffiths, 1990 #77], digested with the appropriate restriction enzyme and Southern blotted onto Zeta-Probe GT under neutral conditions as described by the manufacturer (Bio-Rad). Prehybridizations and hybridizations were carried out in 0.25M Na₂HPO₃/5% SDS at either 65°C (high stringency) or 62°C (moderate stringency). Subsequent washes were carried out for a total of 1 hour in three changes of either 0.5 x SSC (75mM NaCl/7.5mM sodium citrate (pH7.5))/0.1%SDS at 65°C (high stringency) or 1 x SSC/0.1%SDS at 45°C (low stringency).

Results

The plasmid pGT-W contains a 724bp insert that hybridizes to a 4.9kb fragment only in the female great tit. Its DNA sequence was determined (fig.1) and contains a 457bp open reading frame. A search of the EMBL DNA and protein sequence database found no significant matches. The sequence does contain a simple sequence consisting of a 22bp run of thymidines.

The pGT-W insert was used to probe Southern blots, at low stringency, of *PvuII* restricted genomic DNA of male and female great tit, starling (*Sturnus vulgaris*), jackdaw (*Corvus monedula*), pied wagtail (*Motacilla alba*) and a species of new world flycatcher. These are species that cover the extremes of the passeriforme order according to the recent phylogeny of [Sibley, 1988 #409]. In all but the jackdaw convincing hybridization to a single female specific fragment could be observed. In all, species hybridization to one or more non-sex specific

fragments was also shown. A similar experiment was carried out with a non-passerine, the bee-eater (*Merops apiaster*), and this too resulted in faint hybridization to a female specific fragment and two, somewhat stronger bands, in both sexes.

In order to further investigate the nature of the pGT-W insert we attempted to clone a larger fragment of genomic DNA which incorporated this motif. From around 1.5×10^5 plaques from a great tit genomic library, two positives were obtained. After purification one of these gave superior hybridization and was investigated further. The 9.7kb insert was subcloned as pGT1.7 and pGT8 containing 1.7kb and 8 kb respectively. The pGT1.7 was sequenced in its entirety and approximately 2.8kb of the sequence of pGT8 was determined both in only a single direction. A 723bp region, starting 133bp from the 5' end of pGT8 had a sequence that corresponded exactly to the pGT-W insert (fig. 2).

The sequences derived from these subclones were used to search the EMBL database using the FASTA algorithms (GCG, Wisconsin package vers 7.3). A region of 123bp, starting 994bp from the 5' end of pGT8, showed a 79% nucleotide sequence identity to bases 3855-3977 of the mouse *CHD-1* gene (fig. 3)[Delmas, 1993 #415]. This corresponds to an 88% identity at the amino acid level.

Southern blots of *PvuII* digests of genomic DNA from male and female chicken and lesser black-backed gull (*Larus fuscus*) were probed at low stringency with a 433bp *SacI*/*HindIII* fragment of pGT8 that included the 123bp region with *CHD-1* identity (fig. 4). Figure 12 shows that in the chicken hybridization was with a fragment of 3.1kb in the female only and with fragments of 1.5 and 6.0kb in both sexes. In the gull hybridization is similarly with a female specific fragment of 4.0kb a fragment of 3.0kb in males and females.

Delmas *et al.*, (1993) have already demonstrated the universal occurrence of the *CHD-1* in the mammals. The evidence this blot provides, which features species representing both the major divisions of the birds, suggests that a minimum of two types of CHD gene exist in this Class. The first we termed *CHD-W* to denote its W linkage. The 123bp region from the great tit would appear to be a short exon from this gene. The second hypothetical gene is closely related to *CHD-W* and we have it termed *CHD-1A*, where the A denotes its avian nature. This gene is either Z or autosomally linked as it occurs in both sexes.

Isolation of *CHD-1A*

The *SacI*/*HindIII* great tit probe was used at low stringency to screen a lZap II cDNA library from stage 10-12 (33-49hrs after the appearance of the primitive streak) chicken embryos. A plating of 2×10^5 plaques yielded a panel of 25 positive clones, 19 of these continued to hybridize intensely after purification. From three clones Z4, Z6 and Z11 a composite 6313 nucleotide sequence in fig. 5 was determined using the strategy illustrated in fig. 6.

The insert from the Z6 clone (bases 122-4132; fig. 5) and a BglII fragment of the Z4 clone (bases 3763-5007; fig. 5) were used separately to screen a similar number of plaques from a second cDNA library constructed from 10 day old chicken embryos. This screening identified a total of 45 positives of which 16 were found to have sequence identity with the composite sequence derived from the first library. Two additional clones contained a closely related sequence that is dealt with below.

A proportion of the clones from both libraries show variation from the sequence given in fig. 5 in one respect. Clones Z1, Z13, Z17, Z20 and Z23 are identical to the composite sequence 5' to base 4333 from there they terminate in an additional 37 to 163 bases of a new sequence that is identical in all five. Two clones from the second library CC43 and CC56 have 22 or 254bp of the same sequence at their 5' ends. Downstream of this motif both clones regained homology with the composite sequence at base 4334 and show no further deviation from the original sequence. From these seven clones a composite 264bp sequence can be derived and this is illustrated in fig. 7. None of the seven clones contain the whole of this sequence. Moreover, none of the ten clones that span the 4333/4334 insertion point contain this additional region. If inserted at this position the motif has an in frame, open reading frame spanning its entire length. The motif is extremely adenosine rich and this makes the amino acid lysine extremely common in the putative translation (see fig. 7). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing.

Hybridization of a probe running from 2238 to 4132bp of the sequence chicken sequence to a blot of *PvuII* cut, male and female chicken genomic DNA shows that hybridization occurs to fragments that are both W and autosomally or Z chromosomally located. The level of hybridization is significantly stronger to the fragments common to both sexes suggesting that the probe represent the *CHD-1A* gene.

CHD-1A is very closely related to the mouse *CHD-1* gene being 79.8% identical in a 5035nt overlap. At the amino acid level the identity is raised to 90% over 1750 residues. In comparison to the mouse sequence we have yet to obtain the most 68bp 5' of the coding region. We do have an additional 1202bp of the 3' untranslated region but have not encountered a clone with an AATAAA termination signal or a 3' homopolymeric T tail. Both mouse and chicken sequences contain a stop codon in the same relative positions and sequence similarity is insignificant after this point. The published mouse sequence does not contain the additional 264bp motif described above.

The database search also identified an unpublished chicken derived sequence tagged as a delta crystallin binding protein (*DCBP*), with even greater identity than the mouse *CHD-1* gene: 99% over 2293 bp and 94% over 571 amino acid residues. The *DCBP* sequence is of 2292bp which extends over nucleotides 1922 to 4214 of *CHD-1A* (fig. 5). Despite the high nucleotide sequence identity the region of amino acid similarity does not extend the full length of the *DCBP*. This is due to apparent deletions in the *DCBP* clone that provides an initiation

methionine codon (257nt *DCBP*) and a stop codon (1939nt *DCBP*). The extremely high sequence identity, the fact that identity is maintained after the the apparent stop in the *DCBP* sequence, that none of the 41 CHD-related clones we found have exact sequence identity and that only small sequencing mistakes would be required to introduce false stop and start codons suggests that the *DCBP* sequence is *CHD-1A* but has been sequenced slightly inaccurately. Further evidence is required to confirm this however.

The database search with the whole *CHD-1A* gene also revealed significant identity to a previously unidentified portion of a 15 kb region of *S. cerevisiae* chromosome V. This region comprises an open reading frame of 4.4kb which lies between the *RAD4* [Gietz, 1988 #553] and the poly-A binding protein [Sachs, 1986 #554] gene coding regions. In an overlap of 1538 amino acids, the whole of the yeast open reading frame, there is an identity of 37.7% and a similarity of 59% (fig. 10) . The degree of conservation this similarity implies suggests the yeast sequence encodes a homologue of *CHD-1A* that we shall term *CHD-1Y* for the sake of discussion.

Delmas *et al.*, (1993) identified four motifs in *CHD-1* with possible functional significance. *CHD-1A* retains such close homology to *CHD-1* that these regions are virtually unchanged and are likely to perform similar functions as they do in the mouse.

The first motif is a chromodomain [Paro, 1991 #457] which falls between residues 274 and 311 (fig. 9). Figure 11 compares the the amino sequence of this region to that of eight others identified through a search of the EMBL database. The sequences fall into three categories. The first comprises the domain from *CHD-1*, *CHD-1A* and *CHD-1Y*. The second and third chromobox groups have been previously identified by [Pearce, 1992 #424]. The HP1 class comprises the *Drosophila* [James, 1986 #556] and human [Saunders, 1993 #555] *HP1* genes and two murine modifier (*Mod*) genes [Singh, 1991 #420]. The HP1 class is characterized mainly by glutamic acid rich block of six residues upstream of the chromobox. The third group, the Pc class, comprises the *Drosophila Pc* gene [Paro, 1991 #457] itself and its putative murine homologue the *Mod3* gene [Pearce, 1992 #424].

A search of the EMBL data base with the *CHD-1A* putative helicase domain (residues 451-911, fig. 9) raises the identity between this and *CHD-1Y* to 55% in an overlap of 471 amino acids. There is also significant, but lesser identity to, the putative helicase motifs in the human [Okabe, 1992 #558], and *S. cerevisiae* [Laurent, 1992 #454] *SNF2* gene, human [Muchardt, 1993 #557] and *Drosophila Brahma* [Tamkun, 1992 #458], *S. cerevisiae NPS1/STH1* [Laurent, 1992 #454; Tsuchiya, 1992 #560], human excision repair protein *ECCR6* [Troelstra, 1992 #559] and the *RAD54* [Emery, 1991 #562] and *MOT1* [Davis, 1992 #461] genes of *S. cerevisiae*. It should be noted that none of these latter genes contain a chromobox.

Only the four CHD genes show significant homology to the the third motif, a DNA binding region identified by Delmas *et al.*, (1993), whilst only *CHD-1A* and *CHD-1* have the three short basic HSDHR motif near the carboxy terminus, although this region is yet to be sequenced in

CHD-W. The *CHD-1Y* gene apparently terminates before this point so does not share this motif.

Isolation of *CHD-W*

Two, CC14 and CC4, of eight *CHD-1* related clones isolated from the 10 day chick embryo library using 122-4132nt of *CHD-1A* as a probe, overlap (fig. 5) to provide the 1316bp of sequence given in fig. 8. This is a sequence closely related to, but distinct from *CHD-1A*. Identity over the 1316bp overlap is 90.5% and 90.1% at the nucleotide and amino acid level respectively. An alignment of the putative translations of *CHD-1*, *CHD-1A* and *CHD-W* is given in fig. 9. The amino acid identity between *CHD-1* and *CHD-1A* at 93.4% is marginally lower than that between that of *CHD-1* and *CHD-W*, 94.2%, over the same region

The 1335bp insert of CC4 was used at moderate stringency to probe a male/female, *PvuII* cut genomic blot featuring mouse, ostrich (*Struthio camelus*), chicken, bee-eater and hyacinth macaw (*Anodorhynchus hyacinthinus*; fig. 13). Hybridization with the mouse and ostrich shows no evidence of any sex linkage, bands of the same size and equal intensity appearing in both sexes. Hybridization with the ostrich is particularly strong, greater even than with the cognate sequence in the chicken. This suggests that the genome size of the ostrich is considerably smaller than that of the chicken.

In all the bird species apart from the ostrich hybridization occurs with two types of fragment some that are female unique and others that are shared between the sexes. In the chicken some of the latter are of the same size as those hybridizing with the *CHD-1A* probe and result from cross hybridization under the conditions of low stringency that we employed. When probed with the CC4 sequence it is clear that hybridization with the female linked fragments is far stronger, at least in the chicken than with the shared fragments (bear in mind, also, that the female chicken only has a single dosage of the W linked gene). This indicates that CC4 is W linked and represents part of *CHD-W*.

There is also some indication that the intensity of hybridization to the male shared bands is stronger than that to the corresponding female fragments. This suggests that the *CHD-1A* gene is present in different dosages in the two sexes which would result from it being located on the Z chromosome. This remains to be confirmed.

Discussion

The female specific great tit probe GT-W was described by Griffiths and Tiwari (1993) as a means of identifying sex in this species. The results presented here suggest this sequence represents part of an intron in a W linked gene. By moving downstream from this sequence it

has been possible to isolate an putative exon from a gene that we have named *CHD-W* due to its close sequence identity to the mouse *CHD-1* gene [Delmas, 1993 #415] and its W location.

Using the *CHD-W* fragment we attempted to isolate a similar, W linked sequence that Southern blot analysis had shown was present in the chicken. From several clones a 6313bp cDNA sequence was assembled but although it has close sequence identity to the great tit *CHD-W* fragment Southern blot analysis shows it is not located on the W chromosome. This second gene was termed *CHD-1A* (A = avian). This blot shows a second gene closely related to *CHD-1A* is W located. This sequence could not be cloned from a stage 10-12 chick cDNA library although 19 *CHD-1A* clones were isolated. However, two clones yielding ? bp of a second CHD gene were isolated along with a further 14 *CHD-1A* clones from a day 10 chick cDNA library. Southern blot analysis showed that this second clone was W chromosome derived and so represents *CHD-W*. Attempts are underway to isolate the remainder of *CHD-W*.

Southern blots of a variety of bird species showed that *CHD-W* is W chromosome linked in all birds except the ostrich. This suggests that the gene is sex linked throughout the class with the exception of the primitive ratites which the ostrich represents where it appears to be autosomally located.

An alternative explanation is that the *CHD-W* is in fact W linked in ratites but occurs in a region of the W chromosome which still recombines with the Z chromosome. If *CHD-1A* were Z linked, then recombination between Z and W linked copies of CHD would maintain their sequence identity resulting in the apparently autosomal location indicated by the Southern blot. A mammalian example would be the *MIC2* and *STS* genes that are located in the pseudoautosomal region of the Y chromosome [Ellis, 1989 #563] and would give analogous results to those observed here.

Two lines of evidence support this alternative hypothesis. The first is that the Southern blot analysis suggests that *CHD-1A* is Z linked in non-ratites which would make the chromosomal location of the CHD-genes consistent throughout the class. Hybridization of *CHD-1A* to genomic blots is apparently stronger to fragments from male birds which would result from this sex having two copies of any Z linked gene in comparison to a single copy in the female (this result is not clear cut and requires confirmation by chromosomal *in situ*). The second line of evidence is that the sex chromosomes of the ratites are not morphologically differentiated as is the case with other birds [Christidis, 1990 #440]. Morphological similarity suggests recombination still occurs between extensive regions of the ratite Z and W which may include the CHD genes and so produce the pattern of hybridization observed.

Although we have yet to clone the whole of *CHD-1A* the 6313bp sequenced so far shows a close identity to the mouse *CHD-1* gene over the putative coding region. It also includes all four features identified by Delmas *et al.* (1993) as having possible functional significance. This includes a chromodomain, a helicase, a DNA binding motif and a basic, five amino acid motif that is repeated three times (Fig. 9). The similarity of the sequence derived thus far from *CHD-*

W to that of *CHD-1* and *CHD-1A* suggest it will be of similar length and possess these motifs. We have also identified an alternatively spliced form of *CHD-1A* and *CHD-W* which has a similar adenine rich motif inserted at an identical point (nt 4033-4034 *CHD-1A* and nt ? *CHD-W*). The exact form of these alternative mRNAs is yet been elucidated. It is interesting to note that we obtained no clones that spanned these breakpoints which contained this additional motif; the sequence was built up from partial sequences derived from either 5' or 3' termini of different clones. Delmas *et al.*, (1993) produced a mRNA Northern blot probed with fragments of *CHD-1* occurring 5' to this breakpoint and discovered an mRNA species of about 4kb. This would correspond to a species cleaved near this insertion point. What purpose this would serve is unknown. Moreover the putative yeast homologue of *CHD*, *CHD-1Y*, which was identified from amino acid identity to *CHD-1A* from the genomic sequence on the EMBL database does not apparently have a similar motif. This is suggested because the *CHD-1Y* sequence was derived from a genomic clone which would allow the identification of any such sequence were it to be spliced in in the normal manner.

The significance of the four functional domains found in the CHD genes will be discussed in turn. The first, the carboxy-terminal trimer repeat of five basic amino acid residues, has no known function and is not shared by any other sequences from the EMBL database. Furthermore, the *CHD-1Y* gene which is truncated by a little over 200 amino acid residues in comparison to *CHD-1* and *CHD-1A* does not contain this motif.

The second functional domain was identified by Delmas *et al.* (1993) as having sequence selective DNA binding capacity. Whether this is highly specific or just to A+T rich regions was not established. They also noted that this domain contains Lys-Arg-Pro-Lys-Lys and Arg-Gly-Arg-Pro-Arg motifs which enable genes like *HMG-1*, *D1* and *Engrailed* to bind in the minor groove of A+T rich DNA.

A third functional motif is located towards the N-terminus of the CHD-protein and is termed the chromodomain [*Chromatin Organization Modifier*; Paro, 1990 #459]. This is a highly conserved domain of between 37-50 amino acids that has been shown to be represented in the genomes of plants, nematodes, insects and vertebrates [Singh, 1991 #420]. Several chromobox genes have been isolated from human, mouse and *Drosophila* and have been divided into the polycomb (Pc) class and the heterochromatin protein-1 (HP1) class on the basis of related structure [Pearce, 1992 #424]). The CHD-genes have a distinct form of the chromobox characterized by close homology between yeast and vertebrate forms in the 5' half of the box itself but extending a further 17 residues downstream. These differences indicate that this form of the chromobox defines a third subgroup the CHD class

The *Pc* gene forms one of a eponymously named group (Pc-g) of about 12 genes defined through homeotic mutants in *Drosophila* that prevent fixation and maintenance of a determined state. They act as transcriptional repressors of homeotic genes, notably of the antennapedia complex [ANT-C; Paro, 1990 #459]. Members of the ANT-C and the other major group of

Drosophila homeotic genes, the bithorax complex (BX-C), are responsible for defining segmental identity during development [Lewis, 1978 #465; Kaufman, 1980 #464]. Initially, their expression patterns are designated by early acting maternal and segmentation genes (see 4,6,7 kennison). However, these maternal genes are only transiently expressed. During the later stages of development their role as transcriptional activators is adopted by an assemblage of genes including the trithorax group (Trx-g), whilst many of their repressive effects are assumed by the Pc-g [Kennison, 1993 #416].

The *polycomb* (*Pc*) gene itself is perhaps the best studied member of the Pc-g. Zink and Paro (1989) used *Pc-B*-galactose fusion proteins to show that it binds to around 100 different sites on the polytene chromosome including loci where other members of the Pc-g are located. Any disruption of the chromodomain abolishes the specificity of this reaction [Messmer, 1992 #452]. However, the Pc-g protein appears to lack any type of endogenous DNA binding capacity so it is thought that it acts as part of a protein complex with other components that are responsible for the site specific DNA binding [Paro, 1990 #459].

The repressive effects of the Pc-g are are thought to be the result of chromatin compaction. In other words, the DNA is packaged into heterochromatin to prevent or reduce the expression of functional genes [Paro, 1990 #459]. This is a mechanism related to position effect variegation (PEV; [Henikoff, 1990 #460]), to dosage compensation in mammals which sees the complete heterochromatinization of one of the female's X chromosomes and possibly to gene imprinting whereby the expression of maternally and paternally inherited alleles differs [Peterson, 1993 #565]. The links with PEV have recently been substantiated in that HP1, a recognized modifier of PEV, and *Pc* both contain chromodomains [Paro, 1991 #457]. Like the *Pc* protein, HP1 appears to form part of a structural complex that transforms euchromatin to heterochromatin. Furthermore, both PEV and the repressive effects of *Pc* are passed, in a clonal manner, to daughter cells ([Henikoff, 1990 #460; Struhl, 1981 #466]; a characteristic also of gene imprinting.

With the CHD-type gene containing both a DNA binding motif and a chromobox it may appear reasonable to suggest that they encode repressors with an endogenous, site selective DNA binding system. However, CHD genes contain a further functional motif that is structurally related to the helicases. The sequence identity is closest to the yeast *SNF2/SWI2* [Abrams, 1986 #467] and *Drosophila Brahma* genes [Tamkun, 1992 #458], both of which are transcriptional *activators*. Indeed, *Brahma* is part of the Trx-g which are considered direct antagonists to the Pc-g. Other genes which contain more distantly related helicase domains are involved in DNA repair and chromatid separation during mitosis [Laurent, 1993 #453; Sung, 1993 #468].

The *SWI2* gene product has been shown to enhance the transcription of other genes probably as part of a complex that includes *SWI1*, *SWI3*, *SNF5*, *SNF6* and in conjunction with

gene specific DNA binding proteins [Laurent, 1991 #469; Peterson, 1992 #456]. A mode of action strikingly similar to that of *Pc*.

Although it remains to be formally demonstrated that *SWI2* is a helicase, it does have close structural similarities with proven helicase genes and also possesses the required DNA stimulated ATPase activity [Laurent, 1993 #453]. Laurent *et al.*, go on to postulate that the *SWI2* containing complex may act by two mechanisms acting either separately or in conjunction. In the first they envisage helicase mediated DNA melting to allow the egress of RNA polymerase II. Alternatively *SWI2* could allow chromatin remodelling, in effect overcoming any inhibitory packaging of the DNA and so enhancing transcription.

The juxtaposition of a helicase and a chromodomain within the same gene presents a paradox that may challenge the perceived roles of the two motifs. A simple explanation is that alternative splicing could remove one or other of these domains prior to translation. However, there is little support for this idea from the work of ourselves or Delmas *et al.*, (1993).

An alternative explanation could be due to our lack of real knowledge about the function of the chromobox. Whilst it is well established that helicases do disassociate DNA and so facilitate transcription [Matson, 1990 #470], the role of the chromodomain in repression is based on more circumstantial evidence. *Pc*, as we have seen, does not bind DNA itself although mutations in the chromobox prevent the formation of site specific complexes. It is possible that the chromodomain is involved more in maintaining the structural integrity of the repressive complex than in the repressive mechanism itself. Based on this supposition, the CHD-protein may form a different type of complex able to bind at a site dictated or influenced by its own binding domain and activate these loci via helicase activity.

While both this scenario is speculative it is probable that CHD-type genes are active during development and are able to bring about heritable changes in transcription. The presence of an endogenous DNA binding domain suggests it has fewer targets than *Pc*, for example, which could form part of several different active complexes. With *CHD-W* being confined to the W chromosome is likely to have a role in some aspect of female development and we suggest this may be critical to the determination of gender. In support this hypothesis we were unable to find any *CHD-W* clones in a library constructed prior to sex determination which occurs at day 7 [Lutz-Ostertag, 1954 #564] but were able to isolate two clones from a smaller pool of candidates at day 10. This suggests that the expression of *CHD-Y* may occur at a time consistent with it having a sex determining role.

If *CHD-W* alone or in conjunction with *CHD-1A* causes sex determination in birds then then several potential mechanisms are plausible.

(1) In the simplest scenario *CHD-Y* may act as a simple trigger like *SRY* [Koopman, 1993 #550] to either cause expression or repression of downstream genes in order initiate testis development.

(2) *CHD-W* may interact with other autosomal or Z linked genes whereby the dosage of *CHD-W* in comparison these other factors causes initiates development down the male or female pathways.

A more complicated scenario is if *CHD-W* acts in together with *CHD-1A* to cause sexual differentiation. Different mechanisms could operate depending whether *CHD-1A* turns out to be Z linked as we suspect or autosomal.

(3) If *CHD-1A* is Z linked, then male birds get two doses of the *CHD-1A* expression product to one in female birds. Perhaps the 1:1 ratio of functionally distinct *CHD-1A* and *CHD-W* products is what initiates female development whilst a double dosage of *CHD-1A* results in males.

(4) Alternatively, just the single dosage of Z linked *CHD-1A* product could result in female development and expression of *CHD-W* only occurs after sexual differentiation to equalize dosages of functionally similar proteins.

(5) If *CHD-1A* is autosomal however, it could be envisaged that *CHD-1A* and *CHD-W* are functional homologues and the three doses in females (AAW) is required to promote female development, whilst the double dosage in males (AA) causes the differentiation of the testis and the development of the male phenotype.

The evidence from aneuploid chickens discussed in the introduction, does suggest that the mechanism that does operate involves some degree of dosage dependence which tends to exclude mechanism (1). However the similarity of *CHD-W* to *HPI*, the *Pc* protein and other transcriptional modifiers that act through chromatin remodelling show that the expression of this type is crucially dependent on dosage [Locke, 1988 #471]. With the different dosages of gene product and/or potential target sites that aneuploids possess it may be that analysis of these type of mutants has, thus far, served to confuse the issue.

Claims

1. The nucleotide sequences of *CHD-1A* and *CHD-W* as shown in fig. 5, fig. 7 and fig. 8.
2. A clone or subclones of *CHD-1A* and *CHD-W* as defined in 1.
3. A fragment of *CHD-1A* and *CHD-W* capable of giving W specific signal on hybridization to a non-ratite bird.
4. A fragment of *CHD-1A* and *CHD-W* obtainable by restriction endonuclease digestion thereof and being capable of giving a W specific signal on hybridization to genomic DNA of a non-ratite bird.
5. A clone or subclone of a fragment according to either of claims 3 and 4.
6. A nucleic acid or fragment or oligonucleotide having substantially the sequence of *CHD-1A* and *CHD-W* as set out in fig. 5, fig. 7 and fig. 8.
7. A clone or a subclone of a nucleic acid or fragment according to claim 6.
8. A nucleic acid or fragment or oligonucleotide having substantially the same sequence of the chicken or great tit CHD-gene as set out in figs 1, 3, 5, 7 or 8.
9. A nucleic acid or fragment or oligonucleotide being capable of giving a W chromosome specific signal on hybridization to the genomic DNA of a non-ratite bird.
10. A nucleic acid or fragment or oligonucleotide according to claim 4 or claim 9 capable of giving W chromosome specific signal on hybridization to the genomic DNA of a chicken, turkey, duck, parrot.
11. A nucleic acid or fragment or oligonucleotide according to any one of claims 4, 9 and 10 capable of giving W chromosome specific signal on hybridization to the genomic DNA of a non-ratite bird under conditions of high stringency.
12. A nucleic acid or fragment or oligonucleotide according to any one of claims 4, 9 and 10 capable of giving W chromosome specific signal on hybridization to the genomic DNA of a non-ratite bird under conditions of low stringency.
13. A nucleic acid or fragment or oligonucleotide according to any one of the claims 9 to 12 containing substantially the sequence of the chicken CHD-gene as set out in fig. 5, fig. 7 and fig. 8.
14. A nucleic acid or fragment or oligonucleotide encoding a CHD-protein, fragment thereof or polypeptide containing a CHD-gene or part thereof or encoding a CHD-mimotope protein or fragment thereof or CHD-mimotope polypeptide.
15. A process for ascertaining the sex of an embryo, foetus, cell, tissue or organism comprising hybridizing a nucleic acid or fragment or oligonucleotide according to any one of claims 1 to 14 with DNA or RNA of the embryo, foetus, cell, tissue or organism or with cDNA reverse transcribed from RNA of the embryo, foetus, cell, tissue or organism or with cDNA or DNA amplified by cloning or polymerase chain reaction from DNA or RNA of the embryo, foetus, cell, tissue or organism.

16. Use of a nucleic acid or fragment or oligonucleotide of any one of claims 1 to 14 in ascertaining the sex of an embryo, foetus, cell, tissue or organism.
17. A process for controlling the sex of the progeny of an organism comprising inserting a nucleic acid or fragment or oligonucleotide of any one of claims 1-14 into the genome of the organism or progenitor thereof.
18. Use of a nucleic acid or fragment or oligonucleotide of any one of claims 1 to 14 in controlling the sex of the progeny of an organism.
19. A CHD-protein, fragment thereof or polypeptide containing a CHD-gene of part thereof or a CHD-mimotope protein, fragment thereof or a CHD-mimotope polypeptide.
20. A protein or fragment thereof or polypeptide containing a CHD-chromobox including at least one of the characteristic amino acid residues at position 11, 12, 20, 27 or 34 inside the chromobox or 3, 6, 8, 12-15 or 16 directly downstream of the chromobox when aligned to best effect and as set out in fig. 11.
21. A protein or fragment thereof or a polypeptide encoded by a nucleic acid or fragment or oligonucleotide according to claims 1-14 and containing a CHD-chromobox
22. A process for controlling the sex of the progeny of an organism comprising supplying exogenously to a cell of the organism or a progenitor of the organism a protein or fragment thereof or a polypeptide according to any one of claims 19-21
23. A process according to claim 22 wherein the protein or fragment thereof or polypeptide is supplied and activates a *CHD-1A* or *CHD-W* target gene.
24. An antibody or fragment thereof against a protein or fragment thereof or polypeptide according to any one of claims 19-21.
25. An antibody producing cell capable of expressing an antibody or fragment thereof according to claim 24.
26. Use of a protein or fragment thereof or polypeptide according to any one of claims 19-21 or antibody or fragment thereof or cell according to claims 24 or 25 in ascertaining the sex of an embryo cell tissue or organism.
27. A transgenic or chimeric animal having a heterologous nucleic acid or fragment or oligonucleotide according to any one of claims 1 to 14 in the genome of at least the germ cells of the animal.
28. Gametes of an animal according to claim 27.
29. Progeny of an animal according to claim 27.
30. Progeny according to claim 29 which are transgenic or chimeric and have a heterologous nucleic acid or fragment according to any one of claims 1-14 in the genome of at least the germ cells of the progeny.
31. A method of controlling the population of a species of bird which comprises introducing an individual member of the species into the population, said individual having a copy or copies

of a nucleic acid fragment or oligonucleotide according to any one of claims 1 to integrated on a chromosome (carrier chromosome) be it sex linked or autosomal whereby when the male breeds with other individuals of the population the progeny are substantially of one sex or are sexually dysfunctional intersexes.

32. A method according to claim 31 where the nucleic acid integrated into the carrier chromosome is homologous to the native *CHD-1A* or *CHD-W* gene of the bird.

Table 1. Sex of domestic fowl with normal and abnormal chromosome complements (from McCarrey, 1979 #448] and [Crew, 1954 #450])

Chromosome complement	Phenotype
AA ZZ	Male
AA ZW	Female
AA ZZW	Male ?
AA ZZZ	Male
AAA ZZZ	Male
AAA ZZW	Intersex/male

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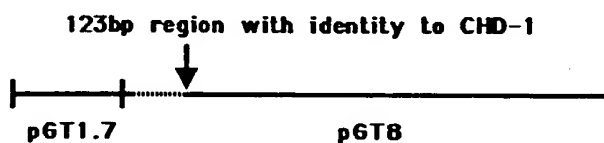
Figure 1. The DNA sequence of the pGT-W insert

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CCCGGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC    60
AAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAAT    120
AATTCTATGAATTCTGTAATTTTATTCTTGATCTTTTGGAGCGAAGTTGTTTGGGGATT    180
TTAGTTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAAACTGACTTTCATTTGCAACATG    240
AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA    300
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTTGGG    360
ATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCTGCCTTCC    420
ATTAATTGCTTGTTTTATGAAACCACTCTTTTTTTTTTTTTTTTTTTTGGCTTCTTCA    480
TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG    540
ATGACAGTGGTACAGGAGCTCTGAATTTTTTTAGATAAACTATGAGAGTGGAACAGAAAT    600
CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACTACATTA    660
GTTGTGTGTTTGAGGAAAAATAAAATGTTTAAGTTGTCCATTCCTTGAAACCTCCCGACC    720
GGG                                                                    723

```

Figure 2. A map of the 9.6kb insert of the lFixII clone isolated from the great tit using pGT-W. pGT1.7 and pGT8 are the two *EcoRI* subclones into which the fragment was divided. The broken line corresponds to the region with absolute sequence identity to the pGT-W insert. The position of the region with identity to the mouse *CHD-1* gene is indicated.

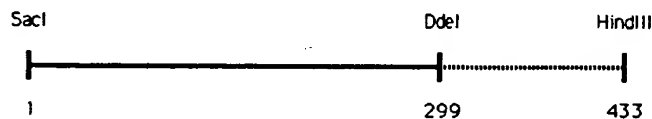


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Figure 3. An alignment of 123bp fragment of the great tit (GT) *CHD-W* gene in pGT8 with the autosomal/Z located chicken (C) *CHD-1A* the chicken *CHD-W* gene and bases 3855-3977 of the mouse (M) *CHD-1* gene. An alignment of the deduced amino acid sequence is also given.

M	<i>CHD-1</i>	ATTCTTCCAG	ATGATCCTGA	TAAAAAACCA	CAAGCAAAAC	AGTTACAGAC	
C	<i>CHD-1A</i>	ATTTTACCTG	ATGATCCAGA	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC	
C	<i>CHD-W</i>	ATTTTACCTG	ATGATCCAGA	TAAGAAACCC	CAGGCTAAGC	AGTTACAGAC	
GT	<i>CHD-W</i>	ATTTTACCTG	ATGACCCAGA	TAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC	
M	<i>CHD-1</i>	CAAAAAACCA	CAAGCAAAAC	AGTTACAGAC	CCGTGCAGAC	TACCTCATCA	
C	<i>CHD-1A</i>	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC	CCGTGCAGAC	TACCTCATTA	
C	<i>CHD-W</i>	CAAGAAACCC	CAGGCTAAGC	AGTTACAGAC	CCGTGCAGAT	TACCTCATTA	
GT	<i>CHD-W</i>	CAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC	CCGTGCAGAT	TACCTCATTA	
M	<i>CHD-1</i>	AACTACTTAG	CAGAGATCTT	GCAAAAAGAG	AGGCTCAGAG	ACTTTGTGGT	GCG
C	<i>CHD-1A</i>	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGCACAAAG	GCTTGCTGGT	GCA
C	<i>CHD-W</i>	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGCACAGAG	ACTTGCTGGT	GCA
GT	<i>CHD-W</i>	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGTGCAAAG	ACTTACTGGT	GCA
M	<i>CHD-1</i>	ILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCGA					
C	<i>CHD-1A</i>	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA					
C	<i>CHD-W</i>	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA					
GT	<i>CHD-W</i>	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEVQRLTGA					

Figure 4. The section of pGT8 that hybridized to a female specific fragment of 3.1kb in the chicken. This probe was also used to screen the chicken cDNA library. The hatched line represents the female specific great tit motif shown in fig. 3.



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Figure 5. A partial nucleotide sequence of *CHD-1A* as defined by the clones Z4, Z6 and Z11.

Two asterisks mark the position where part of the sequence illustrated in fig. 7 is spliced onto the 5' or 3' ends of a proportion of the clones isolated.

GGCTGGGTCA	GCTTCAGGTT	CTGGATCTGG	TTCAAGCTCT	GGAAGCAGTA	GCGATGGAAG	TAGCAGCCAG	TCAGGTAGCA
10	20	30	40	50	60	70	80
GTGACTCTGA	ATCTGGTTCA	GAGTCAGGCA	GTCAATCCGA	ATCAGAGTCT	GACACATCTA	GAGAGAAGAA	ACAAGTTCAA
90	100	110	120	130	140	150	160
GCTAAACCTC	CGAAAGCTGA	CGGATCTGAG	TTTTGGAAGT	CCAGTCCAAG	CATACTTGCT	GTACAGAGAT	CAGCAGTGCT
170	180	190	200	210	220	230	240
CAAGAAGCAA	CAGCAACAGC	AAAAAGCAGC	ATCATCAGAC	AGTGGTTCAG	AAGAGGACTC	ATCCAGTAGT	GAAGATTCTG
250	260	270	280	290	300	310	320
CCGATGATTC	GTCCAGTGAA	ACTAAGAAGA	AAAAGCATAA	AGATGAAGAC	TGGCAAAATG	CAGGGTCAGG	GTCAATATCA
330	340	350	360	370	380	390	400
GGAAGTGGTT	CTGATTCCTGA	ATCGGGCGAA	GATGGGGATA	AAAGCAGTTG	TGAAGAAAGT	GAATCTGACT	ATGAGCCAAA
410	420	430	440	450	460	470	480
AAACAAAGTC	AAAAGCCGTA	AACCTCCAAG	CAGAATTAAG	CCAAAAAGTG	GGAAAAAGAG	CACAGGACAG	AAGAAGAGGC
490	500	510	520	530	540	550	560
AACTTGATTC	ATCAGAGGAG	GAGGAGGACG	ATGATGAAGA	TTATGATAAG	AGAGGATCTC	GTGCGCAGGC	AACAGTGAAT
570	580	590	600	610	620	630	640
GTTAGTTTACA	AAGAAGCTGA	AGAAAACCAAG	ACAGATTCTG	ATGATTTGCT	GGAAGTTTGT	GGAGAGGATG	TCCCACAGAC
650	660	670	680	690	700	710	720
TGAAGAAGAT	GAATTTGAAA	CTATAGAGAA	GTTTATGGAC	AGTCGAATTG	GCCGAAAAGG	AGCCACTGGT	GCCTCAACCA
730	740	750	760	770	780	790	800
CCATCTATGG	CGTTGAGGCA	GATGGTGACC	CAAATGCTGG	GTTTGAAAAG	TCAAAGGAGC	TGGGAGAAAT	ACAGTATCTT
810	820	830	840	850	860	870	880
ATTAAATGGA	AAGGCTGGTC	ACACATCCAT	AACACTTGGG	AAACTGAAGA	AACGCTGAAG	CAACAAAATG	TTAAAGGAAT
890	900	910	920	930	940	950	960
GAACAAATCG	GACAACTACA	AGAAAAGGGA	TCAGGAGACA	AAACGCTGGC	TGAAAAATGC	TTCTCCAGAA	GATGTGGAAAT
970	980	990	1000	1010	1020	1030	1040
ATTATAACTG	CCAGCAGGAG	CTTACAGATG	ATCTGCACAA	ACAATATCAA	ATAGTGGAAA	GAATAATTGC	TCATTCAAAT
1050	1060	1070	1080	1090	1100	1110	1120
CAAAAGTCAG	CAGCTGGTTA	TCCGGACTAC	TATTGCAAAAT	GCCAGGGTCT	GCCTTACTCA	GAATGTAGAT	GGGAAGATGG
1130	1140	1150	1160	1170	1180	1190	1200
TGCTCTCATT	GCCAAAAGT	TTCAGGCACG	CATTGATGAG	TATTTTAGCA	GAAATCAATC	CAAGACTACT	CCCTTTAAGG
1210	1220	1230	1240	1250	1260	1270	1280
ACTGCAAGGT	TCTAAACAG	AGACCAAGAT	TTGTTGCACT	GAAGAAGCAA	CCATCTTACA	TTGGAGGACA	TGAAAGTCTG
1290	1300	1310	1320	1330	1340	1350	1360
GAGTTAAGAG	ATTATCAGTT	AAATGGATTG	AATTGGCTCG	CTCATTCATG	GTGCAAGGA	AATAGTTGTA	TTCTTGACGA
1370	1380	1390	1400	1410	1420	1430	1440
TGAAATGGGT	CTGGGTAAAA	CAATACAAAC	AATTTCTTTT	CTGAACTACC	TGTTTCATGA	ACATCAACTG	TATGGCCCTT
1450	1460	1470	1480	1490	1500	1510	1520
TTCTTCTCGG	CGTGCCACTT	TCTACCTTGA	CATCTTGGCA	AAGAGAGATT	CAAACTTGGG	CTCCTCAGAT	GAATGCTGTA
1530	1540	1550	1560	1570	1580	1590	1600
GTTTACTTAG	GAGATATAAC	TAGTAGAAAT	ATGATAAGGA	CTCATGAATG	GATGCATCCA	CAGACTAAAC	GATTAAAGTT
1610	1620	1630	1640	1650	1660	1670	1680
TAACATACTT	CTGACGACAT	ATGAAATTTT	ACTGAAGGAT	AAGTCATTCC	TTGGTGGTCT	CAATTGGGCA	TTCAATAGGAG
1690	1700	1710	1720	1730	1740	1750	1760
TTGATGAAGC	TCATCGTTTA	AAAAATGATG	ACTCTCTTCT	GTACAGGACT	TTAATAGACT	TTAAGTCCAA	CCATCGACTT
1770	1780	1790	1800	1810	1820	1830	1840
CTGATTACTG	GAACCCCACT	GCAAAATTC	CTCAAGAGC	TGTGGTCTTT	GTTGCATTTC	ATCATGCCAG	AAAAATTTTC
1850	1860	1870	1880	1890	1900	1910	1920
CTCCTGGGAA	GATTTTGAAG	AGGAGCATGG	CAAAGGAAGA	GAGTATGGTT	ATGCAAGTCT	TCACAAAGAG	CTTGAACCAT
1930	1940	1950	1960	1970	1980	1990	2000
TTTTACTAAG	AAGAGTTAAA	AAAGATGTAG	AAAAGTCTTT	ACCTGCTAAG	GTTGAACAAA	TTCTGAGGAT	GGAAATGAGT
2010	2020	2030	2040	2050	2060	2070	2080
GCATTGCAGA	AGCAATATTA	CAAGTGGATT	TTAACAAGGA	ATTATAAAGC	CCTCAGTAAA	GGTTCAAAG	GCAGTACCTC
2090	2100	2110	2120	2130	2140	2150	2160
AGGCTTTCTG	AACATTATGA	TGGAACCTAA	GAAGTGTGT	AACCATTGCT	ACCTCATTAA	GCCACCAGAT	GATAATGAAT
2170	2180	2190	2200	2210	2220	2230	2240
TCTATAATAA	ACAGGAGGCC	TTACAGCAIT	TGATACGTAG	CAGCGGGAAA	CTAATCCTTC	TTGACAAGCT	ACTGATTCGT
2250	2260	2270	2280	2290	2300	2310	2320
CTGCGAGAAC	GTGGCAACAG	AGTTCTGATT	TTCTCTCAGA	TGGTGAGGAT	GCTGGACATC	CTAGCAGAAT	ATCTGAAGTA
2330	2340	2350	2360	2370	2380	2390	2400
TGCGCAGTTT	CCCTTCCAGA	GACTTGATGG	ATCAATAAAA	GGGGAATTGA	GGAAGCAAGC	ACTGGATCAT	TTCAATGCCAG
2410	2420	2430	2440	2450	2460	2470	2480
AAGGATCAGA	GGATTTCTGT	TTTTTACTGT	CTACAAGAGC	TGGAGGATTA	GGTATTAACT	TGGCATCTGC	TGACACTGTA
2490	2500	2510	2520	2530	2540	2550	2560
GTTATTTTGT	ATTCTGACTG	GAATCCACAG	AATGATCTGC	AGGCACAGGC	GAGAGCTCAT	AGAATTGGAC	AGAAGAAACA
2570	2580	2590	2600	2610	2620	2630	2640
GGTTAATATT	TATCGGCTAG	TCACAAAAGG	ATCAGTAGAA	GAAGATATTC	TTGAAAGAGC	CAAGAAGAAG	ATGGTGCTAG
2650	2660	2670	2680	2690	2700	2710	2720
ACCATTTAGT	AATTCAGAGA	ATGGACACGA	CAGGAAAAAC	TGTTCTGCAT	ACAGGTTCAA	CTCCATCAAG	CTCTACACCT

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2730	2740	2750	2760	2770	2780	2790	2800
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2810	2820	2830	2840	2850	2860	2870	2880
JCCCCAGGAA	ATGGATATAG	ATGAAATCTT	GAAGAGAGCT	GAAACTCGGG	AAAATGAGCC	AGGTCCATTG	ACTGTAGGGG
2890	2900	2910	2920	2930	2940	2950	2960
ATGAGTTGCT	TTCACAGTTC	AAGGTGGCGA	ACTTTTCCAA	TATGGATGAA	GATGATATTG	AGTTGGGAAC	AGAAAGAAAT
2970	2980	2990	3000	3010	3020	3030	3040
TCAAGAAAT	GGGAAGAAAT	CATCCCAGAA	TCCCAACGGA	GAAGGATAGA	GGAGGAGGAA	AGACAAAAG	AACTTGAAGA
3050	3060	3070	3080	3090	3100	3110	3120
AATATACATG	CTCCCAGGGA	TGAGAAACTG	TGCAAAACAG	ATCAGCTTTA	ATGGGAGTGA	AGGAAGACCC	AGTAGGAGCA
3130	3140	3150	3160	3170	3180	3190	3200
GAAGATATTC	TGGATCTGAT	AGTGACTCCA	TCACAGAAAG	AAAACGGCCA	AAAAGCGGTG	GAAGACCTCG	AACCATTCCT
3210	3220	3230	3240	3250	3260	3270	3280
CGAGAAAATA	TTAAAGGATT	TAGTGATGCA	GAGATCAGGC	GGTTTATCAA	GAGTTACAAG	AAATTGGGTG	GCCTCTCGGA
3290	3300	3310	3320	3330	3340	3350	3360
AAGGTTAGAT	GCTGTAGCTA	GAGATGCTGA	ACTGGTTGAT	AAATCTGAGA	CAGACCTTAG	ACGTTTGGGT	GAACTTGTAC
3370	3380	3390	3400	3410	3420	3430	3440
ATAATGGATG	CATTAAGGCT	TTAAAGGACA	ATTCATCTGG	ACAAGAAAGA	GCAGGAGGTA	GACTTGGGAA	AGTTAAAGGC
3450	3460	3470	3480	3490	3500	3510	3520
CCAACGTTTC	GAATCTCAGG	AGTGCAAGTG	AATGCAAAAC	TAGTCATCTC	TCACGAGGAA	GAGCTGGCAC	CAGTGCACAA
3530	3540	3550	3560	3570	3580	3590	3600
ATCCATTCTC	TCAGATCCAG	AAGAAAGGAA	AAGATATGTC	ATCCCATGCC	ACACCAAGGC	TGCTCACCTC	GATATAGATT
3610	3620	3630	3640	3650	3660	3670	3680
GGGTAAAGA	AGATGATTCC	AATCTGTTAG	TAGGCATCTA	TGAATATGGC	TATGGCAGCT	GGGAAATGAT	AAAAATGGAT
3690	3700	3710	3720	3730	3740	3750	3760
CCAGATCTCA	GCTTAACACA	GAAGATTTTA	CCTGATGATC	CAGACAAGAA	ACCCAGGCA	AAGCAGCTAC	AGACCCGTGC
3770	3780	3790	3800	3810	3820	3830	3840
AGACTACCTC	ATTAAATTAC	TGAATAAAGA	CCTTGCAAGA	AAGGAAGCAC	AAAGGCTTGC	TGGTGCAGGC	AATTCCAAGA
3850	3860	3870	3880	3890	3900	3910	3920
GAAGGAAGAC	AAGAAATAAG	AAGAATAAGA	TGAAGGCTTC	AAAAATAAAA	GAAGAAATAA	AGAGTGATTC	TTACCACAA
3930	3940	3950	3960	3970	3980	3990	4000
CCCTCAGAAA	AATCTGATGA	AGATGATGAG	GAGGAGGATA	ACAAGGTAAA	TGAAATGAAA	TCTGAAATAA	AAGAAAAATC
4010	4020	4030	4040	4050	4060	4070	4080
TAAAAAAATT	CCATTGCTGG	ATACTCCAGT	TCATATTACT	GCAACCAGTG	AACCAGTTCC	TATCTCAGAA	GAATCTGAAG
4090	4100	4110	4120	4130	4140	4150	4160
AACTCCATCA	GAAGACATTT	AGTGTGTGCA	AAGAAAGAAAT	GAGGCTGTCT	AAAGCAGCAC	TGAAACAGCT	GGATAGACCA
4170	4180	4190	4200	4210	4220	4230	4240
GAGAAGGGCC	TTTCTGAAAG	GGAGCAGCTG	GAACATACTA	GGCAGTGTCT	AATCAAAATT	GGGGATCACA	TTACAGAAATG
4250	4260	4270	4280	4290	4300	4310	4320
CCTGAAGGAG	TACACAAATC	CCGAGCAAAT	AAAACAGTGG	AGGAAAAAAT	TGTGGATTTT	TGTGTCCAAG	TTTACAGAAAT
4330	4340	4350	4360	4370	4380	4390	4400
TTGATGCCAG	AAAGCTGCAC	AAACTCTACA	AACATGCAAT	CAAAAAGCCG	CAAGAGTCTC	AGCAACACAA	TGACCAAAAC
4410	4420	4430	4440	4450	4460	4470	4480
ATTAGCAGCA	ATGTGAATAC	ACATGTAATC	AGAAATCCAG	ATGTGGAAAG	ACTGAAGGAG	ACTACAAACC	ATGATGATAG
4490	4500	4510	4520	4530	4540	4550	4560
TAGCAGGGAC	AGTTATTCTT	CTGATAGACA	TTTATCACAA	TACCATGATC	ATCACAAAGA	CAGGCATCAG	GGAGATGCTT
4570	4580	4590	4600	4610	4620	4630	4640
ACAAGAAAAG	TGACTCCAGG	AAAAGGCCAT	ATTCAAGCTT	CAGTAATGGA	AAAGATCACA	GAGACTGGGA	TCACTACAAA
4650	4660	4670	4680	4690	4700	4710	4720
CAGGACAGCA	GATACTACAG	TGATAGTAAA	CATAGAAAGT	TAGATGACCA	CAGGAGCAGA	GACCCAGAGT	CAAACCTGGA
4730	4740	4750	4760	4770	4780	4790	4800
AGGAAACTTA	AAAGACAGCC	GGGGTCATTC	AGATCACCGC	TCCCATTTCAG	ACCACAGGAT	ACACTCAGAT	CACCCGTCCA
4810	4820	4830	4840	4850	4860	4870	4880
CTTCAGAAAT	CAGCCATCAT	AAATCTTCGA	GAGATTATAG	ATACCACATCA	GACTGGCAAA	TGGACCACAG	AGCTTCTGGT
4890	4900	4910	4920	4930	4940	4950	4960
AGTGGCCCGA	GGTCACCACT	AGATCAGAGG	TCTCCTTATG	GTTCAAGATC	TCCCCTAGGA	CACAGATCTC	CATTTGAACA
4970	4980	4990	5000	5010	5020	5030	5040
CTCATCAGAT	CACAAAAGTA	CACCTGAACA	TACATGGAGT	AGCCGGAAGA	CATAACAAAG	ACTGACATTT	TCTGGACCTT
5050	5060	5070	5080	5090	5100	5110	5120
CTTTTTCAGC	ATATACAGTA	AACTAACACA	GTAATTGCCT	TACATGACTT	GAAAGATATG	GACTGGATAT	TCTATCAGTA
5130	5140	5150	5160	5170	5180	5190	5200
GCAATATGTT	TACTTCTTTC	CAGGATGCAA	GGTCTATTAT	CCCAACAGAA	GAAAAATATT	TTTGTATTTA	AAGTTTATGC
5210	5220	5230	5240	5250	5260	5270	5280
TGCACTGTGC	TGCAAAATGTT	GTGGCATTTC	TTTTTTAAGA	AATGGAAGAT	GTTTACTTTT	ACAGGACCTT	CAACACTGCC
5290	5300	5310	5320	5330	5340	5350	5360
CCTTTCAGAC	TGGATCTTAC	TATAAACTC	TTCATGTCAA	AGTGGTTCTA	GGCTGAACAC	AGATTAAATT	ATGTTTGTAA
5370	5380	5390	5400	5410	5420	5430	5440
ATGAACACTT	AAACACTGAC	CTGTGCTTAT	GTTTCAGGAA	AGAATGGGGG	ATTTATTTTG	TTTTATTTC	TGGTAGAGAA
5450	5460	5470	5480	5490	5500	5510	5520
CTCTCAAGGA	CTTTGTTTAC	TTTCCAAAGC	TACTTGTTTA	CATGTGTACAC	TGCGACCAAC	TTGCCGCTTT	TCATCACAAG
5530	5540	5550	5560	5570	5580	5590	5600
CTTGAAATAT	TAAATCTCTG	ACCTACAGTT	GTAATAATAG	CAGGATTCTCT	CCTGTTTGTG	ATCAGTTATA	ATGCCTTTTT
5610	5620	5630	5640	5650	5660	5670	5680
ATGAACAAA	CAACAAACA	AAAAACAAT	AAAAAAAATA	ACACAACAAA	ACCAACAAT	GGCTGTAAAT	TATTGTAAAT
5690	5700	5710	5720	5730	5740	5750	5760
TAATTAATG	AGCTTTTTC	CGTCAGGCTT	TTTTTGCGTG	TTCTTTTCCC	CAACAACCTCA	GGCCTTCTTT	TCACAAGTTC
5770	5780	5790	5800	5810	5820	5830	5840

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AGTATACTTA	CATGTTTTAA	TAAAATATCT	CGATGGAATC	AGAATGTAAA	AATGGGGAAG	GGAATATTTT	ATTCCATTTA
5850	5860	5870	5880	5890	5900	5910	5920
GTGCTCCTTT	TTTATGGGAT	ACTTTTACAT	ACCTGTTTTT	GGTGTGTTTA	TTTTATTTTT	TTTTTCTATT	AAACTGTCAG
5930	5940	5950	5960	5970	5980	5990	6000
TGTTGTGATT	GTGTAAATGA	ACAGTGAGAA	TATCCCACTC	TAAACTGTGC	CCTGGAAAGC	TTTTCAGGTG	CATTGGTTTA
6010	6020	6030	6040	6050	6060	6070	6080
AAAGAAGGAA	GTGTTCTATA	GGTGAACACT	TCAAAACCCA	GATCAGCCAA	GATTCATTGT	AAATCCATTT	GTTTTCCCTC
6090	6100	6110	6120	6130	6140	6150	6160
TTTAACATGG	GCAATAATGT	CAAATGTGCT	ATGCAGCAGT	TAATATTTTA	GAAGATTGA	ATGACTTTAT	TAACAGAATT
6170	6180	6190	6200	6210	6220	6230	6240
GTTACAATGC	ACACTGATTG	TACATAGATA	ACTTCTATCT	GACAAATTAA	ATTAACTAAA	ACCAAAAAAA	ACC
6250	6260	6270	6280	6290	6300	6310	

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Figure 6. The strategies used to determine the nucleotide sequence of *CHD-1A* and *CHD-W* given in fig. 5 and fig. 8. The top line represents the mouse clone given by [Delmas, 1993 #415]. The three 'Z' clones of *CHD-1A* and the 'CC4' and 'CC14' clones of *CHD-W* were derived from either a stage 10-12 or a 10 day chick cDNA library respectively. Arrows indicate the direction of sequence determination.

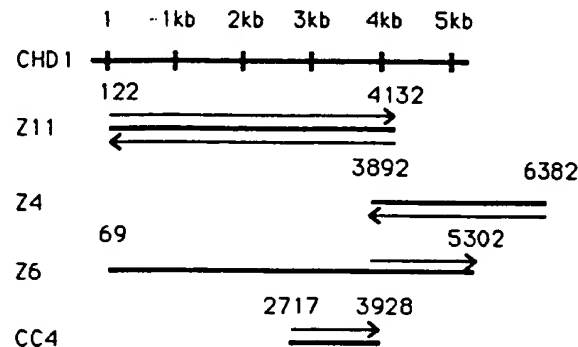


Figure 7. A composite nucleotide sequence and putative translation of the motif that is found spliced to a proportion of the 5' or 3' termini of *CHD-1* clones or the 3' end of the *CHD-W* clone CC14.

		D E I V S V K H L E K K I K T E
<i>CHD-1A</i>	1	GATGAGATTGTTTCAGTGAAACATCTACATAAAAAATAAAAAACAGAAA
<i>CHD-W</i>	1	GATGGGATTGTTTCAGTGAAACATCCACATAAAAAATAAAAGCAGAAA
		D G I V S V K H P H K K I K A E
		K E N E E K P E P D I G I K K E A
<i>CHD-1A</i>	51	AAAGAAAATGAAGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCT
<i>CHD-W</i>	51	AAAGAAAATGAAGAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT
		K E N E E K D E P E I G I K K E A
		E E K R E T K E K E N K R E L K R
<i>CHD-1A</i>	101	GAAGAAAAAGAGAGACAAAAGAGAAGGAAAAATAAAAGGAATTGAAAAGG
<i>CHD-W</i>	101	GGAGAAAAAGAGAGACAAAAGAAAAGGAAAAATAAGA
		G E K R E T K E K E N K
		E K K E K E D K K E L K E K D N K
<i>CHD-1A</i>	151	GAGAAAAAGAAAAGAGGATAAGAAAGAATTAAAAAGAAAAGATAATAAA
		E K R E N K V K E S T Q K E K E V
<i>CHD-1A</i>	201	GAAAAGAGAGAAAACAAAGTAAAAGAATCCACACAGAAAGAAAAGAAAGTG
		K E E K
<i>CHD-1A</i>	251	AAGGAAGAGAAG

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Figure 8. A partial nucleotide sequence of *CHD-W* as defined by the clones CC4 and CC14.

ATTATCGGC	TAGTCACAAA	AGGATCAGTA	GAAGAAGATA	TTCTTGAAG	AGCCAAGAAA	AAGATGGTGT	TAGATCATT
10	20	30	40	50	60	70	80
AGTGATTGAG	AGAATGGACA	CCACAGGGAA	AACGTGACTA	CATACAGGCT	CTACTCCTTC	AAGCTCAACA	CCTTTTAATA
90	100	110	120	130	140	150	160
AGGAAGAGTT	ATCAGCAATT	TTGAAGTTTG	GTGCTGAGGA	ACTTTTAAAA	GAACCTGAAN	NNGAAGAAGA	GGAGCCTCAG
170	180	190	200	210	220	230	240
GAGATGGATA	TAGATGAAAT	CCTGAAGAGG	NCTGAACTC	GAGAAAAATGA	GTCAGGCCCA	TTAACTGTAG	GAGATGAGTT
250	260	270	280	290	300	310	320
ACTTTCACAG	TTCAAGGTAG	CTAACTTTTC	CAATATGGAT	GAAGATGACA	TTGAATTGGA	ACCAGAACAA	AATCTAAGAA
330	340	350	360	370	380	390	400
ACTGGGAAGA	AATCATTTCCA	GAAGTTCAGT	GGCGACGAAT	AGAGGGGNG	GAAAGACAAA	AAGAACTTGA	AGAAATATAT
410	420	430	440	450	460	470	480
ATGCTTCCAA	GAATGAGAAA	CTGTGCAAAA	CAGATCAGCT	TTAATGGAAA	TGAAGGGAGA	TGCAGTAGGA	GCAGAAGATA
490	500	510	520	530	540	550	560
TTCTGGATCT	GATAGTGATT	CCATCTCAGA	AAGAAAACGA	CCAAAAAAC	GTGGACGACC	ACGAACATAT	CCCCGTGAAA
570	580	590	600	610	620	630	640
ACATTAAAGG	ATTAGTGAT	GCAGAGATTA	GACGATTTAT	CAAGAGTTAC	AAGAAATTG	GTGGCCCACT	TGAAAGGTTA
650	660	670	680	690	700	710	720
GATGCTATAG	CTAGAGATGC	TGAGCTAGTT	GATAAATCTG	AAACAGACCT	TAGACGCTG	GGAGAAGTTG	TACATAATGG
730	740	750	760	770	780	790	800
ATGCATTAAAG	GCTTTAAATG	ATAATGACTT	TGGTCAAAGGA	AGAACAGGTG	GTAGATTGCG	GAAAGTTAAA	GGCCCAACAT
810	820	830	840	850	860	870	880
TCCGAATAGC	AGGAGTGCAG	GTGAATGCAA	AGCTAGTCAT	TTCTCAGGAA	GAAGAGTTGG	CACCATTGCA	TAAATCGATT
890	900	910	920	930	940	950	960
CCTTCAGATC	CAGAAGAAAG	GAAAAGATAT	GTCATCCCAT	ACCACACCAA	AGCAGCTCAT	TTTGATATAG	ATTGGGGTAA
970	980	990	1000	1010	1020	1030	1040
AGAAGATGAT	TOCAATCTGT	TAATAGGCAT	CTATGAATAT	GGTTATGGCA	GTTGGGAAAT	GATAAAAAATG	GATCCTGATC
1050	1060	1070	1080	1090	1100	1110	1120
TCAGTTTGAC	ACAGAAGATT	TTAAGTGATG	ATCCAGATAA	GAAACCCAG	GCTAAGCAGT	TACAGACTCG	TGCAGATTAC
1130	1140	1150	1160	1170	1180	1190	1200
CTCATTAAAT	TACTGAATAA	AGACCTTGCA	AGAAAGGAAG	CACAGAGACT	TGCTGGTGCA	GGCAATTCAA	AGAGGAGAAA
1210	1220	1230	1240	1250	1260	1270	1280
AACAAGAAGT	AAGAAGAATA	AAGCAACAAA	GGCTGCAAAA	AAAAA			
1290	1300	1310	1320	1330			

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Figure 9. An alignment of the deduced amino acid sequences of the chicken (C) *CHD-1A* and mouse (M) *CHD-1*. With gaps introduced to maximize alignment they show a sequence identity of 91.8% over 1339 residues. The \$ sign indicates start and stop codons. Boxed sections are the chromodomain (C), Helicase, (H) and the region containing the DNA binding domain (B) identified by Delmas *et al.*, (1993). A trimer repeat of a basic HSDHR motif is underlined. A* denotes residue identity and . similarity.

C <i>CHD-1A</i>	-----	\$
M <i>CHD-1</i>	PFALCPVVTQREPQETRECRKFIFEILIFEICITHLLLLIGDFCFINFLIFTMNGHSDE	
C <i>CHD-1A</i>	-----AGSASGSGSGSSSGSSSDGSSSQSGSSDSGSGSGSGSQSESSED	
M <i>CHD-1</i>	ESVRNGSGESSQSGDDCGSASGSGSGSSSGSSSDGSSSQSGSSDSGSGSDSGSQSESSED	
	*****.***.*****	
C <i>CHD-1A</i>	TSREKKQVQAKPPKADGSEFWKSSPSILAVQSAVLKKQOQQ--QKAASSDSGSEEDSS	
M <i>CHD-1</i>	TSRENK-VQAKPPKVDGAEFWKSSPSILAVQSAVLKKQOQQQAPASSNSGSEEDSS	
	****.* *****.*****.***.*****	
C <i>CHD-1A</i>	SSEDSADDSSSETKKKKHKDEDWQMSGSGSVSGTGSDESSEAEDGKSSCEESESSEDPKN	
M <i>CHD-1</i>	SSEDS-DDSSSGAKKKKHNDEDWQMSGSGSPQLGSDSESEKEDKSSCDGTESSEDPKN	
	*****.***.*****.*****.*****.*****	
C <i>CHD-1A</i>	KVKSRRPPSRKPKSGFKSTGQKKRQLDSSEEEEDDEDYDKRGSRRQATVNVSYKEAKE	
M <i>CHD-1</i>	KVRSRKPQNRKSKNGKKILGQKKRQIDSSEDEDEDYDNDKRSRRQATVNVSYKEDEE	
	..*.***.*****.*****.***.***.*****	
C <i>CHD-1A</i>	TKTDSDDLLEVCGEDVPQTEDEFETIEKFMDSRIGRKATGASTTIYAVEADGDPNAGF	
M <i>CHD-1</i>	MKTDSDDLLEVCGEDVPQPEDEEFETIERVMDCRVGRKATGATTTIYAVEADGDPNAGF	
	*****.***.*****.*****.*****.*****.*****	
C <i>CHD-1A</i>	EKSKEIGSIQYLKWKGWSHIHTWETETLKQONVKGHNKLDNYKKKQETKRWLNAS	
M <i>CHD-1</i>	ERNKEFGDIQYLKWKGWSHIHTWETETLKQONVKGHNKLDNYKKKQETKRWLNAS	
	..*****.*****.*****.*****.*****	
C <i>CHD-1A</i>	PEDVEYYNCQQLTDDLEKQYQIVERILASNQSAAGYPDYCKWQGLPYSECSWEDGA	
M <i>CHD-1</i>	PEDVEYYNCQQLTDDLEKQYQIVERILASNQSAAGLPDYCKWQGLPYSECSWEDGA	
	*****.*****.*****.*****.*****.*****.*****	
C <i>CHD-1A</i>	LIKKFQARIDEYFSRNQSKTTPFKDCKVLKQRPFRFVALKKQPSYIGGHEGLELRDYQLN	
M <i>CHD-1</i>	LISKFPQTCIDEYFSRNQSKTTPFKDCKVLKQRPFRFVALKKQPSYIGGHEGLELRDYQLN	
	..*****.*****.*****.*****.*****	
CHD	GLNWLASWCKGNCSILADEMGLKTIQTISFLNYLFHEBQLYGPFLLRVPLSTLTWQR	
MCBOX	GLNWLASWCKGNCSILADEMGLKTIQTISFLNYLFHEBQLYGPFLLVPLSTLTWQR	
	*****.*****.*****.*****.*****.*****.*****	
CHD	EIQTWAPQMNNAVYVLGDIISRNMIRTHEWMHPQTKRLKFNILLTYEILLKDKSPLGGLN	
MCBOX	EIQTWASQMNNAVYVLGDIISRNMIRTHEWMHPQTKRLKFNILLTYEILLKDKAPLGGLN	
	*****.*****.*****.*****.*****.*****.*****	
CHD	WAFIGVDEAHLKNDSDLLYRTLIDFKSNHRLITGTPLQNSLKEWLSLLHFIMPEKFPSS	
MCBOX	WAFIGVDEAHLKNDSDLLYKTLIDFKSNHRLITGTPLQNSLKEWLSLLHFIMPEKFPSS	
	*****.*****.*****.*****.*****.*****.*****	
CHD	WEDFEEEBGKGREYGYASLEKELEPFLRRVKKDVEKSLPAKVEQILRMESALQKQYK	
MCBOX	WEDFEEEBGKGREYGYASLEKELEPFLRRVKKDVEKSLPAKVEQILRMESALQKQYK	
	*****.*****.*****.*****.*****.*****.*****	
CHD	WILTRNYKALSKSGKSTSGFLNIMMELKCCNHCYLIKPPDNEFYKQALQHLIRSS	
MCBOX	WILTRNYKALSKSGKSTSGFLNIMMELKCCNHCYLIKPPDNEFYKQALQHLIRSS	
	*****.*****.*****.*****.*****.*****.*****	
MCBOX	GKLILLDKLLIRLRERGNRVLIFSQVMRMLDILAEYLKYRQFFQRLDGSIKGEIRKQAL	
CHD	GKLILLDKLLIRLRERGNRVLIFSQVMRMLDILAEYLKYRQFFQRLDGSIKGEIRKQAL	
	*****.*****.*****.*****.*****.*****.*****	
MCBOX	DEFNAGSEDFCFLLSTRAGGLGINLASADTVVIFDSWNPQNDLQAQARAHRIGQKKQV	
CHD	DEFNAGSEDFCFLLSTRAGGLGINLASADTVVIFDSWNPQNDLQAQARAHRIGQKKQV	
	*****.*****.*****.*****.*****.*****.*****	

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Figure 10. An alignment of the deduced amino acid sequences of *CHD-1a* and *CHD-1Y* a putative yeast homologue of the chicken gene identified through a search of the EMBL data base. With gaps introduced to maximize alignment they show a sequence identity of 37.7% over 1538 residues. | indicates identity and : conservative substitution.

```

55 KPPKADGSEFWKSSPSILAVQSAVLKKQQQQAASSDSSGSEEDSSSSE 104
   .::|.::|...|:::..|.....|..|:::|:|
2654 MAAKDISTEVLQN.PELYGLRRS...HRAAAHQQNYFNDSDEDD....E 2695
   |.::|... ..|::|.....:::|:|:|...|:|
105 DSADDSSSETKKKKHKDEDWQMSGSGSVSGTGSDESAAEDGKSSCEESE 154
   |.::|... ..|::|.....:::|:|:|...|:|
2696 DNIKQSRKRMTTIEDDED.....EFEDEEGEEDSGEDEDEEDFEEDD 2738
   |:..|...|...|...|...|...|...|...|...|...|...|...|
155 SDYEPKNKVKSRKPPSRIPKSGKSTGQKKRQLDSSEEEEDDEDYDKR 204
   .|:..|...|...|...|...|...|...|...|...|...|...|...|
2739 DYYGSPKQNRSKPKSRTKSKSKPKSQSEKQSTVKIP.....TRF 2780
   |:..|...|...|...|...|...|...|...|...|...|...|...|
205 GSRRQATVNVSYKEAETKTDSDDLLE....VCGEDVPQT....EEDEF 246
   :|..|...|...|...|...|...|...|...|...|...|...|...|
2781 SNRQNKTVNYNIDYSDDDLLESEDDYGSEELSEENVHEASANPQPEDFH 2830
   |:..|...|...|...|...|...|...|...|...|...|...|...|
247 TIEKFMDSRIGRKATGASTTIYAVEADGPNAGFEKSKELGEIQYLIKW 296
   .|:..|...|...|...|...|...|...|...|...|...|...|...|
2831 GIDIVINERL.....KTSLEEGKVLEKTVPDNLNCKE..NYEFLIKW 2870
   |:..|...|...|...|...|...|...|...|...|...|...|...|
297 KGWSBIHNTWETEETLRQONVKGMNKLDNYKKK...DQETKRWLKNASPE 343
   .:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
2871 TDESHLENTWETYESIGQ..VRGLKRLDNYCKQFIIEDQVRLDPYVTAE 2918
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
344 DVEYYNCQQLTDDLHKQYQIVERIIA..HSNQSAAGYPDYCKWQGLP 391
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
2919 DIEIMDERERRLDEFEEFHVPERIIDSQRASLEDGTSQLOLVKWRRLN 2968
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
392 YSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKDCKVLKQRPFRVALK 441
   |..|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
2969 YDEATWENATDIVKLAPEQVKHFQNRNSKILPQYSSNYTSQRPREFKLS 3018
   |..|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
442 KOPSYIGGHESLELRDYQLNGLNWLASHWCKGNSCILADEMGLGKTIQTI 491
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
3019 VQPPFIKGG...ELRDFQLTGINWMAFLWSKGDNGILADEMGLGKTVQTV 3065
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
492 SFLNYLFHEHQLYGPFLLRVPLSTLTWQREIQTWAPQMNAVYVYLGDITS 541
   .|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
3066 AFISWLIFARRQNGPHIIVVPLSTMPAWLDTFEKWAPDLNCICYMGNQKS 3115
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
542 -RNMIRTHEW....MHPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGV 587
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
3116 RDTIREYEFYTNPRAGKKTMTKFNVLTTTYEYILKDRALGSIKWQFMAY 3165
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
588 DEAHRLKNDSSLRYRTLIDFKSNHRLITGTPLQNSLKELWSLLBFIMPE 637
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
3166 DEAHRLKNAESSLYESLNSFKVANRMLITGTPLQNNIKELAAVLNFLMPG 3215
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
638 KFSSWEDFE.EEHGKGREYGYASLHKELEPFLLRVVKDVEKSLPAKVEQ 686
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
3216 RFTIDQEIDFENQDEEQEYIHDLEHRIQPFILRLKKDVEKSLPSKTER 3265
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
687 ILRMEMSALQKQYKWILTRNYKALSKGSGSTSGFLNIMMELKKCCNHC 736
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
3266 ILRVELSDVQTEYKNIILTKNYSALTAGAKGGHPSLLNIMMELKKASNP 3315
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
737 YLIKPPDDNEF.....YNKQELQBLIRSSGKLIILLKLLIRLRERGN 779
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
3316 YLFDNAEERVLOKFGDGKMTRENVLRGLIMSSGKMVLLDQLLTRKKDGH 3365

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780	RVLIFSQVMRMLDILAEYLKYRQFPFQRLDGSIGELRKQALDFNAEGS	829
3366	RVLIFSQVMRMLDILGDYLSIKGINFQRLDGTVPASQRRISIDBFNSPDS	3415
830	EDFCFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKK	879
3416	NDFVFLSTRAGGLGINLMTADTVVIFDSDWNPQADLQAMARAHRIGQKN	3465
880	QVNIYRLVTKGSVEEDILERAKKKMVLDELVIQRMDDTGKTVLBTGSTPS	929
3466	HVMVYRLVSKDVTVEEVLERARKKMILEYAIISLGVTDGKNKYTKKNEP..	3513
930	SSTPFNKEELSAILKPGAELFKPEPEGEEQEPQEMDIDEILKRAETRENE	979
3514NAGELSAILKFGAGNMFTATD.NQKKLEDLNLDDVLNHAEDHVT	3557
980	PG...PLTVGDELLSQFKVANFSNMDEDDIELEPERNSRNWEEIIPESQR	1026
3558	PDLGESHLGGEFLKQFEVTDY.....KADIDWDDIIPPEEL	3594
1027	RRIEEEERQKELEE.....IYMLPRMRNCAQOI..SFNGSE.....	1060
3595	KKLQDEEQKRKDEEYVKEQLEMNRRDNALKKIKNSVNGDGTAAANSDD	3644
1061	..GRRSRSRYSGSDSDSITERKRPKKRGRPRTPR.ENIKGFS...AE	1104
3645	DSTSRSSRRRARANDMSIGE...SEVRALYKAILKFGNLKEILDELIAD	3691
1105	IRRFIKSYKKFGGPLERLDAVARDA.....ELVDKSETDLRRLGEL	1145
3692	GTLPVKSFEKYGETYDEMMEAAKDCVHEEERNRKEILEKLEKHATAYRAK	3741
1146	VHNGCIKALKD.NSSQGERAGRLGKVKGPTFRISGVQ.VNAKLVISHEE	1193
3742	LKSGEIKAENQPKDNPLTRLSLKKREKKAFLNFVKGVKSLNAESLLSRVE	3791
1194	ELAPLHKSIPSD.PEERKRYVIPCHTKAA..HFDIDWGKEDDSNLLVGII	1240
3792	DLKYLKNLINSNYKDDPLKFSLGNNTPKPVQNWSSNWTKEEDEKLLIGVF	3841
1241	EYGYGSWEMIKMDPDLSTQKILPDD.....	1266
3842	KYGYGSWTQIRDDPFLGITDKIFLNEVHNPVAKKSASSSDTTPPSKKKGK	3891
1267PDKKPQAKQLQTRADYLIKLLNKDLARK.....EAQRLAGAGNS	1305
3892	GITGSSKKVPGAIBLGRRVDYLLSFLRGGLNTPSPSADIGSKKLPTGPSK	3941
1306	KRRKTRNKKNMKASKIKEEIKSDSSQPSEKSDDEDEE...EDKNVNM	1352
3942	KRQRKPANHSKSMTEPITSSSEPANGPPSKRMKALPKGPAALINNTRLSPN	3991
1353	KSENKEKSKKIPLDTPVHITATSEPVPISSEELHQTFVSVCKERMMP	1402
3992	SPTPLKSKVSRDNGTR....QSSNPSSGSAHEKEYDSMDEEDCRBTMSA	4037
1403	VKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECLKEYTNPEQIKQ	1452
4038	IRTSLKRLRRGGKSLDRKEWAKILKTELTTIGNHI.ESQKGSSRKASPEK	4086
1453	WRKNLWIFVSKF..TEFDARKLHKLYKHAIKKRQESQQ	1488
4087	YRKELWSYSANFWPADVKSTKLAMY....DKITESQK	4120

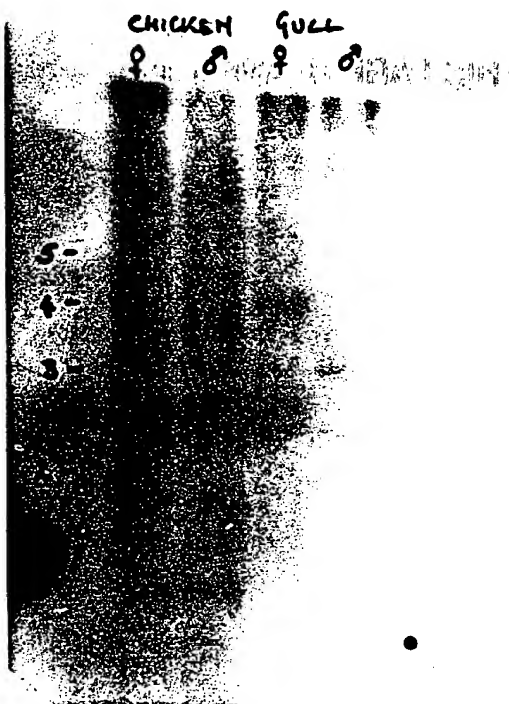
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Figure 11. Comparison of 9 chromodomain sequences. Vertical lines indicate the extent of the chromodomain as defined by [Paro, 1991 #457]. The top three sequences represent the CHD class of chromodomain to add to the HP1 class and Pc classes as defined by [Pearce, 1992 #424]. The first letter of each annotation indicates the animal of origin: C, chicken; M mouse; D, Drosophila; H, human; Y, *S. cerevisiae* whilst the remainder identifies the gene type. The yeast gene is a possible CHD homologue identified by its close identity to the vertebrate forms. * indicates sequence identity within the groups and ^ identity between all nine sequences. _ indicate amino acid residues inside and downstream of the motif that are characteristic of the CHD class chromobox.

CCBD	AVEAD	GDPNAGFEKSKELGE.IQYLIKWKGWSHINTWETEET	LKQONVKG MNKLDNYKK
MCHD	AVEAD	GDPNAGFERNKEPGD.IQYLIKWKGWSHINTWETEET	LKQONVRGNK KLDNYKK
YCHD	EGKVL	EKTVPDLNNCKE..N.YEFLIKWTDESHLENTWETYES	IGQ..VRGLKRLDNYCK
		** **** ** *****	* * * *****
DHP1	EEEE	YAVEKIIDRRVRK GK.VEYLLKWKGY PETENTWEPENN	LDCQDLIQQY
HHP1	EDEE	YVVEKVLDRRVVKGKQVEYLLKWKGFSEEHTWEPEN	LDCPELISEF
MMOD1	EEEE	YVVEKVLDRRVVKGK.VEYLLKWKGFSDENTWEPENN	LDCPDLIAEF
MMOD2	AEPE	FVVEKVLDRRVVNGK.VEYFLKWKGFTDADNTWEPENN	LDCPELIEDF
	**	*** **** ** ***** *****	*** **
DPC	PVDLV	YAAEKIIQKRVRKGV.VEYRVKWKGNQRYNTWEPENN	ILDRRLIDY
MMOD3	VGEQV	FAAECILSKRLRK GK.LEYLVKWRGWSSKHSWEPEEN	ILDPRLLLAF
	*	*** * ** *** ** ***** *****	*****
		^^ ^ ^^	

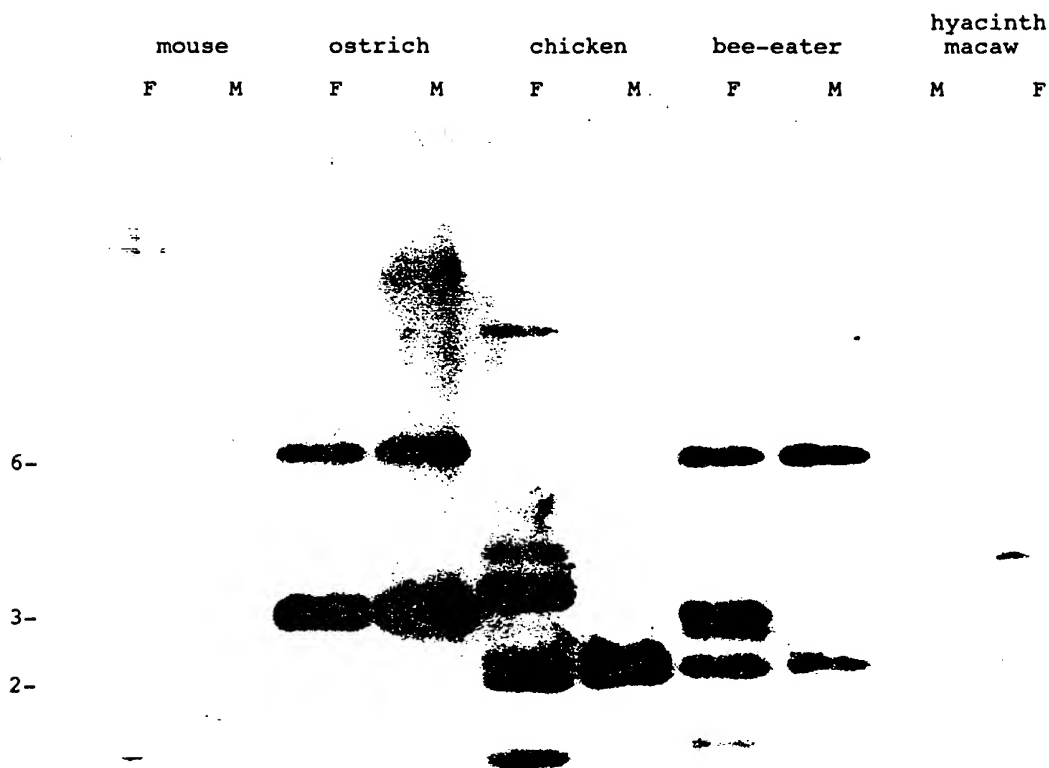
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Figure 12. Genomic Southern blots of DNA from male and female chickens and lesser black-backed gulls digested with PvuII and probed with a 433bp HindIII/Sac fragment of pGT8 (fig 4.) at moderate stringency. Hybridization with female linked fragments and fragments common to both sexes can be observed in both species. Numbers give approximate sizes in kilobases.



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Figure 13. Genomic Southern blots of DNA from male (M) and female (F) mice, ostrich, chicken, bee-eater and hyacinth macaw probed with the 1335bp insert of CC4 at moderate stringency. Hybridization with mouse and ostrich is with fragments shared by both sexes whilst the non-ratite birds show additional hybridization to female specific fragments. In these latter species, the signal from female linked hybrids is stronger than with autosomal/Z linked fragments indicating that the probe is derived from the W chromosome. Numbers give approximate sizes in kilobases.



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